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(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypep-  
tides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

DESCRIPTION  
PROTEIN KINASES

FIELD OF THE INVENTION

5           The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

10           The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

          Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key  
15           biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

          Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following:  
20           cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the  
25           etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

          The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moiety modulates protein function in multiple ways. A common mechanism  
30           includes changes in the catalytic properties ( $V_{\max}$  and  $K_m$ ) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the



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ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex  
5 activates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also been recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) *Science* 283:1325-1328). A third important  
10 outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) *Genes Dev* 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several  
15 hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple  
20 alignment of the sequences in the catalytic domain of protein kinases and subsequent parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

We have recently completed a systematic analysis of the protein kinases present in  
25 *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), *Proc. Natl. Acad. Sci.* 96:13603-13610).

30 Using parsimony analysis, the protein kinases may be divided into 4 major groups: AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungus-specific kinases, and a family designated "other" to represent several smaller families. In addition, we designate an "atypical" family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

5 The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca<sup>2+</sup>/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain  
10 kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, microtubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

15 CMGC group kinases are "proline-directed" enzymes phosphorylating residues that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

20 The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptosis.

Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EIFKs); homologues of the  
25 yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close  
30 homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD\_sp, YGR262\_sc) kinases, and others that are "unique" and don't cluster into any obvious family.

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### SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting

SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
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SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
5 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides  
conjugated to each other, including DNA and RNA, that is isolated from a natural source  
10 or that is synthesized. The isolated nucleic acid of the present invention is unique in the  
sense that it is not found in a pure or separated state in nature. Use of the term "isolated"  
indicates that a naturally occurring sequence has been removed from its normal cellular  
(i.e., chromosomal) environment. Thus, the sequence may be in a cell-free solution or  
placed in a different cellular environment. The term does not imply that the sequence is  
15 the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at  
least) of non-nucleotide material naturally associated with it, and thus is distinguished  
from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the  
specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of  
20 the total DNA or RNA present in the cells or solution of interest than in normal or  
diseased cells or in the cells from which the sequence was taken. This could be caused by  
a person by preferential reduction in the amount of other DNA or RNA present, or by a  
preferential increase in the amount of the specific DNA or RNA sequence, or by a  
combination of the two. However, it should be noted that enriched does not imply that  
25 there are no other DNA or RNA sequences present, just that the relative amount of the  
sequence of interest has been significantly increased. The term "significant" is used to  
indicate that the level of increase is useful to the person making such an increase, and  
generally means an increase relative to other nucleic acids of about at least 2 fold, more  
preferably at least 5 to 10 fold or even more. The term also does not imply that there is no  
30 DNA or RNA from other sources. The other source DNA may, for example, comprise  
DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term  
distinguishes from naturally occurring events, such as viral infection, or tumor type

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growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

5 It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The  
10 claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from  
15 the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately  $10^6$ -fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

20 By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,  
25 SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,  
30 SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

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5 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,  
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SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,  
10 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,  
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,  
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional  
15 derivatives thereof as described herein. For sequences for which the full-length sequence  
is not given, the remaining sequences can be determined using methods well-known to  
those in the art and are intended to be included in the invention. In certain aspects,  
polypeptides of 100, 200, 300 or more amino acids are preferred. The kinase polypeptide  
can be encoded by a full-length nucleic acid sequence or any portion of the full-length  
20 nucleic acid sequence, so long as a functional activity of the polypeptide is retained. By  
“functional” domain is meant any region of the polypeptide that may play a regulatory or  
catalytic role as predicted from amino acid sequence homology to other proteins or by the  
presence of amino acid sequences that may give rise to specific structural conformations  
(*i.e.*, coiled-coils). For some purposes, polypeptide domains are preferred, including, but  
25 not limited to, N-terminal, catalytic/kinase and C-terminal.

The amino acid sequence will be substantially similar to a sequence selected from  
the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID  
NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID  
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID  
30 NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID  
NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID  
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID

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NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID  
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15 NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID  
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID  
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NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID  
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding  
20 full-length amino acid sequence, or fragments thereof. A sequence that is substantially  
similar to a sequence selected from the group consisting of those set forth in SEQ ID  
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ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 or portions of or the entire corresponding full-length amino acid sequences.

By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the above calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402), Blast2 (Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) *J. Mol. Biol.* 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID

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5 NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID  
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NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID  
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NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID  
NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will  
15 have at least 75% identity (preferably 90%, more preferably at least 95% and most  
preferably 99-100%) to the sequence selected from the group consisting of those set forth  
in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID  
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID  
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID  
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5 NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID  
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID  
NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID  
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID  
NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c)  
10 hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes  
a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an  
amino acid sequence selected from the group consisting of those set forth in SEQ ID  
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
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NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
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NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ  
25 ID NO:242, except that it lacks one or more, but not all, of a domain selected from the  
group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a  
coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-  
terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a  
polypeptide having an amino acid sequence selected from the group consisting of those set  
30 forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID  
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID  
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NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID  
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID  
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID  
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID  
20 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID  
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID  
NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or  
fragments thereof. (The domain demarcations of the polypeptides of the invention are  
indicated in Table 2 by reference to the kinase domain.) A sequence that is substantially  
25 similar to a sequence selected from the group consisting of those set forth in SEQ ID  
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID  
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID  
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID  
30 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID  
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID  
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID

NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ



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ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of

those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,

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SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240,  
SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%,  
more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide  
selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,  
5 SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,  
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,  
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,  
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,  
SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,  
10 SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,  
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SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,  
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SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,  
15 SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,  
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,  
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,  
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,  
SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,  
20 SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,  
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,  
SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,  
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,  
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,  
25 SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,  
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the  
domain is selected from the group consisting of an N-terminal domain, a catalytic domain,  
30 a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region,  
an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h)  
encodes a polypeptide having an amino acid sequence selected from the group consisting

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of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID  
NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID  
NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID  
NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID  
5 NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID  
NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID  
NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID  
NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID  
NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID  
10 NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID  
NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID  
NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID  
NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID  
NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID  
15 NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID  
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NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID  
20 NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID  
NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID  
NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID  
NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID  
NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID  
25 NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino  
acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence  
selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,  
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,  
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,  
30 SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,  
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,  
SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,

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SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,  
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,  
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5 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,  
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,  
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,  
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,  
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,  
10 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,  
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SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at  
20 least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-  
100%) to the sequence selected from the group consisting of those set forth in SEQ ID  
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID  
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID  
25 NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID  
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID  
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID  
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID  
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID  
30 NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID  
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID  
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

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NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID  
NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID  
5 NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID  
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID  
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID  
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID  
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID  
10 NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID  
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID  
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID  
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ  
ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under  
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NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID  
NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID  
20 NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID  
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID  
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID  
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID  
NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID  
25 NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID  
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID  
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID  
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID  
NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID  
30 NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID  
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID  
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID

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NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,

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SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the



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complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) *J. Biol. Chem.* 270, 29071-29074). The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein the N-terminal domain can be identified.

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation).

5 The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further,  
10 in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

15 The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate  
20 after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

25 The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine amino acids. The molecule may be another protein or a polypeptide.

30 The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal

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domain may play a regulatory role is PAK3 which contains a heterotrimeric G<sub>i</sub> subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) *Nature*, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) *Meth. Enzymology* 266:513-525). Coiled-coils are formed by two or three amphipathic  $\alpha$ -helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) *Science* 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) *J. Biol. Chem.* 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

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sequence analysis programs such as the DNASTar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein-protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000).

Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not be the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

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The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM  $\text{NaH}_2\text{PO}_4$ , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

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vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

The term "vector" relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

The term "transfecting" defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field, detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term "promoter" as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes, the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID



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NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID  
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID  
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID  
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID  
5 NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID  
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID  
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID  
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID  
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID  
10 NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ  
ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative  
thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a  
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID  
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID  
15 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID  
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID  
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID  
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID  
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID  
20 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID  
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID  
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID  
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID  
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID  
25 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID  
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID  
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID  
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID  
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID  
30 NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID  
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID  
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

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NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,

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SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,  
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,  
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,  
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,  
5 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,  
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,  
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,  
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,  
10 SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,  
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,  
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,  
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,  
15 SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,  
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,  
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,  
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,  
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
20 SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof.  
25 In particular, a unique nucleic acid region is preferably of mammalian origin and  
preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of  
nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is  
selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,  
30 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,  
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,  
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,  
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,  
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,  
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,  
5 SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,  
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,  
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,  
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,  
10 SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,  
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,  
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,  
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,  
15 SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,  
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
20 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid  
probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino  
acid sequence selected from the group consisting of those set forth in SEQ ID NO:122,  
SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,  
25 SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132,  
SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137,  
SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,  
SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147,  
SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152,  
30 SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157,  
SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162,  
SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167,

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SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,  
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177,  
SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,  
SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,  
5 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
10 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
15 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe  
contains a nucleotide base sequence that will hybridize to a sequence selected from the  
group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ  
ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9,  
20 SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ  
ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID  
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25,  
SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ  
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID  
25 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41,  
SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ  
ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID  
NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57,  
SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ  
30 ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID  
NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73,  
SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

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NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in *Nonisotopic DNA Probe Techniques*, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,  
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,  
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,  
5 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
10 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the  
genomic regulatory elements, or may be under the control of exogenous regulatory  
elements including an exogenous promoter. By "exogenous" it is meant a promoter that is  
15 not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase  
polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid  
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID  
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID  
20 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID  
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID  
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID  
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID  
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID  
25 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID  
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID  
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID  
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID  
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID  
30 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID  
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID  
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID



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NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence. By "fragment," is meant an amino acid sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
5 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-  
length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase  
polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ  
10 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ  
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ  
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ  
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ  
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ  
15 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ  
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ  
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ  
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ  
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ  
20 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ  
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ  
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ  
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ  
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ  
25 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ  
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ  
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ  
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ  
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ  
30 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ  
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ

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ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (e.g., in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

5 In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, 10 20 25 30 the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

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amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

5 ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ  
ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ  
ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ  
ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ  
ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ  
ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ  
ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ  
ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ  
ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ  
10 ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ  
ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ  
ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ  
ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ  
ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ  
15 ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ  
ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ  
ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ  
ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ  
ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ  
20 ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ  
ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ  
ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group  
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ  
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ  
25 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ  
ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ  
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ  
ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ  
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ  
30 ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ  
ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ  
ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

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ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
NO:242 where the domain is selected from the group consisting of an N-terminal domain,  
a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich  
region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence  
15 selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,  
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,  
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,  
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,  
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,  
20 SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,  
SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,  
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,  
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,  
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,  
25 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,  
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,  
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,  
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,  
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,  
30 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,  
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,  
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,



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SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,  
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,  
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,  
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,  
5 SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it  
lacks one or more, but not all, of the domains selected from the group consisting of a C-  
terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich  
10 region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain  
demarcations of the polypeptides of the invention are indicated in Table 2 by reference to  
the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in  
the art. The natural source may be mammalian, preferably human, blood, semen, or tissue,  
15 and the polypeptide may be synthesized using an automated polypeptide synthesizer. The  
isolated, enriched, or purified kinase polypeptide is preferably selected from the group  
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ  
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ  
ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ  
20 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ  
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ  
ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ  
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ  
ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ  
25 ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ  
ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ  
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ  
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ  
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ  
30 ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ  
ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ  
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,

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SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By "recombinant kinase polypeptide" is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By "specific binding affinity" is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term "specific binding affinity" describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term "polyclonal" refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

"Monoclonal antibodies" are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term "antibody fragment" refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

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kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and where the domains are defined as above. By "hybridoma" is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a kinase of the invention. In preferred embodiments, the antibody to the kinase comprises a sequence of amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

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SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
NO:242. The binding agent is preferably a purified antibody that recognizes an epitope  
present on a kinase polypeptide of the invention. Other binding agents include molecules  
that bind to kinase polypeptides and analogous molecules that bind to a kinase  
15 polypeptide. Such binding agents may be identified by using assays that measure kinase  
binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a  
kinase polypeptide of the invention or an equivalent sequence. The method involves  
identifying the novel polypeptide in human cells using techniques that are routine and  
20 standard in the art, such as those described herein for identifying the kinases of the  
invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR  
amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that  
modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide  
25 selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,  
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,  
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,  
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,  
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,  
30 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,  
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,  
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,  
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,  
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,  
5 SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,  
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,  
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,  
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,  
10 SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,  
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,  
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
15 SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b)  
measuring the activity of said polypeptide; and (c) determining whether said substance  
modulates the activity of said polypeptide.

20 The term "modulates" refers to the ability of a compound to alter the function of a  
kinase of the invention. A modulator preferably activates or inhibits the activity of a  
kinase of the invention.

The term "activates" refers to increasing the cellular activity of the kinase. The  
term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is  
25 preferably the interaction with a natural binding partner.

The term "modulates" also refers to altering the function of kinases of the  
invention by increasing or decreasing the probability that a complex forms between the  
kinase and a natural binding partner. A modulator preferably increases the probability that  
such a complex forms between the kinase and the natural binding partner, more preferably  
30 increases or decreases the probability that a complex forms between the kinase and the  
natural binding partner depending on the concentration of the compound exposed to the



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kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

5 The term "complex" refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

10 The term "natural binding partner" refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

15 The term "contacting" as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

20 In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, 25 SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, 30 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,  
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,  
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,  
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
5 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,  
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,  
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,  
SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
10 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
15 and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change  
in cell phenotype or the interaction between said polypeptide and a natural binding  
partner.

The term "expressing" as used herein refers to the production of kinases of the  
invention from a nucleic acid vector containing kinase genes within a cell. The nucleic  
20 acid vector is transfected into cells using well known techniques in the art as described  
herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal  
condition by administering to a patient in need of such treatment a substance that  
modulates the activity of a polypeptide selected from the group consisting of SEQ ID  
25 NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID  
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID  
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID  
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID  
30 NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID  
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID  
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID

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NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question. Substances that modulate the activity of the polypeptides

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preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term "preventing" refers to decreasing the probability that an organism contracts or develops an abnormal condition.

5 The term "treating" refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

The term "therapeutic effect" refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of  
10 abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating  
15 efficacy against abnormal conditions can be identified as described herein.

The term "abnormal condition" refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, *i.e.*, irregularities in  
20 normal cell cycle progression through mitosis and meiosis.

Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

Abnormal differentiation conditions include, but are not limited to  
25 neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the  
30 protein kinases could lead to cell immortality or premature cell death.

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The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

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5 ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ  
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ  
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ  
ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ  
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ  
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ  
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ  
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ  
ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ  
10 ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ  
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ  
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ  
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ  
ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ  
15 ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ  
ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ  
ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe  
comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the  
complements of the sequences and fragments; and (b) detecting the presence or amount of  
20 the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from  
the group consisting of rheumatoid arthritis, arteriosclerosis, autoimmune disorders, organ  
transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative  
stress-related neurodegenerative disorders, metabolic disorder including diabetes,  
25 reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group  
consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID  
NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ  
ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID  
30 NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20,  
SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ  
ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

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NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID  
NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID  
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID  
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID  
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID  
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID  
NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID  
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID  
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID  
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID  
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID  
NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID  
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID  
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID  
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID  
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID  
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID  
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding  
full-length amino acid sequence, or a functional derivative thereof. Hybridization  
conditions should be such that hybridization occurs only with the kinase genes in the  
presence of other nucleic acid molecules. Under stringent hybridization conditions only  
highly complementary nucleic acid sequences hybridize. Preferably, such conditions  
prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20  
contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the  
genes in the presence of other nucleic acid molecules. Under stringent hybridization  
conditions only highly complementary nucleic acid sequences hybridize. Preferably, such  
conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20  
contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic  
include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in  
comparison to normal cells. By "amplification" is meant increased numbers of kinase



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DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

"Amplification" as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon

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& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative  
10 publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5,316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris  
15 *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*,  
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); and Sikora *et al.*, Analytical Biochem. 172:344-355 (1988), all of which are incorporated  
25 herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432  
30 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., "J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Biol. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

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formulated in animal models to achieve a circulating concentration range that initially takes into account the  $IC_{50}$  as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows:

1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, Journal of American Veterinary Medical Assoc., 202:229-249, 1993).

Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in  
10 a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID  
15 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID  
20 NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID  
25 NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID  
30 NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

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NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting  
5 differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include,  
10 but are not limited to, those discussed previously.

The term "comparing" as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine  
15 these discrepancies in sequences are well-known to one of ordinary skill in the art. The "control" nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the  
20 narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred  
25 embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

### BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID



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NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34,  
SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ  
ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID  
NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50,  
5 SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ  
ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID  
NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66,  
SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ  
ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID  
10 NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82,  
SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ  
ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID  
NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98,  
SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103,  
15 SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108,  
SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113,  
SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118,  
SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

## DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding  
such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides,  
assays utilizing such polypeptides, and methods relating to all of the foregoing. The  
present invention is based upon the isolation and characterization of new kinase  
25 polypeptides. The polypeptides and nucleic acids may be produced using well-known and  
standard synthesis techniques when given the sequences presented herein.

### I. The Nucleic Acids of the Invention

Included within the scope of this invention are the functional equivalents of the  
30 herein-described isolated nucleic acid molecules. The degeneracy of the genetic code  
permits substitution of certain codons by other codons that specify the same amino acid  
and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID

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5 SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,  
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SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,  
10 SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,  
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SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
15 SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded  
by the nucleotide sequence. For example, the present invention is intended to include any  
nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-  
end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA,  
20 TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or  
its derivative. Moreover, the nucleic acid molecule of the present invention may, as  
necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-  
end.

Such functional alterations of a given nucleic acid sequence afford an opportunity  
25 to promote secretion and/or processing of heterologous proteins encoded by foreign  
nucleic acid sequences fused thereto, for example. All variations of the nucleotide  
sequence of the kinase genes of the invention and fragments thereof permitted by the  
genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with  
30 codons other than degenerate codons to produce a structurally modified polypeptide, but  
one which has substantially the same utility or activity as the polypeptide produced by the  
unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

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functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

5           Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins.  
10          Therefore, these nucleic acid molecules are also part of the invention.

          The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore  
15          presumably define new protein kinase groups.

          Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

## 20          II.     Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

          A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory,  
25          Sambrook, Fritsch, & Maniatis, eds., 1989).

          In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain  
30          reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

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radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

### III. DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.



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Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells. Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include  $\gamma$ gt10,  $\gamma$ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage  $\lambda$ , the *bla* promoter of the  $\beta$ -lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage  $\lambda$  ( $P_L$  and  $P_R$ ), the *trp*, *recA*, *lacZ*, *lacI*, and *gal* promoters of *E. coli*, the  $\alpha$ -amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the  $\zeta$ -28-specific promoters of *B. subtilis* (Gilman *et al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic

promoters are reviewed by Glick (Ind. Microbiot. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987; Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).

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Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (Mol. Cell. Biol. 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

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the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEI, pSC101, pACYC 184,  $\pi$ VX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). *Bacillus* plasmids include pC194, pC221, pT127, and the like (Gryczan, In: *The Molecular Biology of the Bacilli*, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as  $\phi$ C31 (Chater *et al.*, In: *Sixth International Symposium on Actinomycetales Biology*, Akademiai Kiado, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, Miami Wntr. Symp. 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, Cell 28:203-204, 1982; Bollon *et al.*, J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: *Cell Biology: A Comprehensive Treatise*, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

#### IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

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 SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
 10 SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
 NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of  
 these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-  
 15 terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are  
 provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI,  
 CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant  
 number of protein kinases that do not belong to any of the known groups, and therefore  
 20 presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1,  
 Table 2, Table 3 and Table 4, provided below.

#### V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein 25 Kinases

The present invention relates to an antibody having binding affinity to a kinase of  
 the invention. The polypeptide may have an amino acid sequence selected from the group  
 consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ  
 ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ  
 30 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ  
 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ  
 ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

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5 ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ  
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ  
ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ  
ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ  
ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ  
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ  
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ  
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ  
ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ  
10 ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ  
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ  
ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ  
ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ  
ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ  
15 ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ  
ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ  
ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ  
ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ  
ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ  
20 ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or  
at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more  
contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the  
polypeptide not provided in the sequences above, but that is present in the full-length  
sequence of the polypeptide and that is easily obtained using methods standard in the art.  
25 Further, the antibody may bind specifically to particular domains of one or more of the  
kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or  
C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to  
a kinase or kinase domain of the invention. Such an antibody may be isolated by  
30 comparing its binding affinity to a kinase of the invention with its binding affinity to other  
polypeptides. Those that bind selectively to a kinase of the invention would be chosen for  
use in methods requiring a distinction between a kinase of the invention and other



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polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or  $\beta$ -galactosidase) or through the inclusion of an adjuvant during immunization.

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For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, *see* Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engval *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromatography.

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Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

#### VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

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The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

5 The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions  
10 is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit  
15 the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S.  
20 Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*).

25 Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

30 Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

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Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

## VII. Biological Significance, Applications and Clinical Relevance of Novel Protein

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### Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-catalytic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or therapeutic utility for each of the proteins.

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The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune, neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

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The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatinum, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

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Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevalent tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

5       Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

      Tumor associated: Mok (SEQ ID NO:57), EPK2, AA316804 (SEQ ID NO:11), AA435956 (SEQ ID NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

      Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

15       Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

      Neuronal restricted: CAMKKB (SEQ ID NO:66)

      Hematopoietic expressed: PTK9L (SEQ ID NO:22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

20       Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP\_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

      Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

#### VIII. Transgenic Animals.

      A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (e.g., the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (*Experientia* 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO<sub>2</sub> asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, *Cell* 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.

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Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

#### IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro*, and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

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1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

5 In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is  
10 precipitated with  $\text{CaPO}_4$  and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and  
15 particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to  
20 solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic acid molecule into a cell. Gene transfer is commonly performed to enable the expression  
25 of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or  
30 receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

#### X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

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takes into account the  $IC_{50}$  as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

5 Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by  
10 altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used);  
15 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

20 At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc.*, 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross  
25 necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

### EXAMPLES

10 The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

#### EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases Materials and Methods Identification from cDNA databases and isolation of clones encoding novel protein kinases

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Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

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Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

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with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

	ID#	ID#	Parent	5' primer	3' primer
sp	na	aa	Sequence	Sequence*	Sequence*
H	33	153	2R22-5-11	GAGATCGRNTTYAARGA RTTYGA	TGTCACNCCNAGNSWCCAN AYRTT
M	81	200	5R57_10_2_ m TESK2_m	GCTGCTGGACAGTGACT TGTATIT	GAAAGCAAAGCCTTCACAC CTT
H	67	187	5R69_17_2_h	CTCTCACCTCAGGAAC GG	GCTTGCGGATCTTCTCA
H	46	166	SGK309_h	GACATCCTGCCGGCCAA CTACG	CGGCCCTGGAGCTGCATCA CTA
M	67	228	5R72_16_2_h	TGCGCGACACCATTGAC CAG	CTCAGGGCTTACATACAGA G
H	45	165	5R72_8_2_h	AAAGGAGAACTACATT TGAAAAAT	CTTCATCATCTCTAATACAT TGGTTGG
H	41	161	Z36720	CAAATTAAGATCATTGA CTTTGGG	GGAAACAAAGTCCTTGGCC TC
H	115	234	AL031652 - Pak6	GTGGACATCTGGTCCCT CG	GTAGGTCCTTCACTCTTGG AG

- degenerate oligonucleotide residue designation:

5 N= A,C,G or T

R= A or G

Y= C or T

S = C or G

W= A or T

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#### Full-length sequence extension of protein kinases using cDNA and genomic databases

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1. The gapped blast algorithm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

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PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

Database	Database Date
LifeGold templates	Feb 2000
LifeGold compseqs	Feb 2000
LifeGold compseqs	Mar 2000
LifeGold compseqs	Apr 2000
LifeGold fl	Feb 2000
LifeGold flt	Apr 2000
NCBI human Ests	May 2000
NCBI murine Ests	May 2000
NCBI nonredundant	May 2000

5

Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNASTar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.

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The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (<http://www.sanger.ac.uk/Software/Wise2/>) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

Database	Number of entries	Database Date
Celera v. 1-5	5,306,158	Jan 19/00
Celera v. 6-10	4,209,980	Mar 24/00
Celera v. 11-14	7,222,425	Apr 24/00
Celera v. 15	243,044	May 14/00
HGP all Genescan	25,885	Apr 04/00
HGP; Phase 0	4,944	May 04/00
HGP; Phase 1	28,478	May 05/00
HGP; Phase 2	1,508	May 04/00
HGP; Phase 3	9,971	May 05/00

#### Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the *evc* (AJ250839) (ellis-van creveld syndrome and weyers acrodermal dysostosis) gene from 4p16.1.

5 Human 5R79-46-1\_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-length gene for the TANK-binding kinase (TBK1) (Pomerantz, J.L. and Baltimore, D. (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF- $\kappa$ B activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

15 Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

20 Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceeded by the sequence

25 "RGLLAPGDPPCPPNPAPATPPSSRLPTLFSNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

30 Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

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region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

5 Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKCnu (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

10 Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102  
15 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

20 Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM\_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

25 Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema, H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1 ) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

30 Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi, T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM\_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324\_h orthologue of W30246\_m (SEQ ID NO:24, SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP\_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte.7249119\_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

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refer to the aa sequence of the closest homolog (RU2S, NP\_057440) used for the Smith-Waterman query): N-term from Incyte 6010175\_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175\_2, Celera 17000030058129 (241-262 DCX homology).

5 Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides 1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three  
10 inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to  
15 encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838\_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135\_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from  
20 Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735\_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135\_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte  
25 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on  
30 blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

5 Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015\_m (SEQ ID NO: 42, SEQ ID NO:162)

10 tBlastn analysis identified KIAA1297 (AB037718). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

15 The full-length ORF for R19772 was isolated by screening a cDNA library using a probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

20 Table 8. Isoforms for R19772

Kestrl Name	Kestrl AA Acc #	Isoform type	Source	Description*
Trad (Duet)	R19772	B	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762
		C	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762



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				Deletion of 32 aa (160-191)
		D	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)
		E	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)

\* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

5 Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3\_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

10 Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

15 Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

20 Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

25 Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredundant public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5,787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NR database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344\_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)

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Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478\_m (SEQ ID NO:80, SEQ ID NO:199)

5 Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

10 The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

15 Table 9. Isoforms for AA232253

Kestrl Name	Kestrl AA Acc #	Isoform type	Description*
MLK4	AA232253	MLK4	Substitution of C for W at 346
		MLK4B	Different Cterm (332-800); seq in MLK4B is as shown in *

\* C-terminus specific to MLK4B

20 LPLAARMSEESYFESKTEESNSAEMSCQITATSN GEGHGMNPSLQAMMLMGFGDI  
FSMNKAGAVMHSGMQINMQAKQNSS  
KTTSKRRGKKVNMA LGFSDFDLSEGDDDDDDGEEEDNDMDNSE

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

25 Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

5 Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

10 Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

15 Human SGK022 orthologue of AA060026\_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

20 Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence 1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

25 Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

30 Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 (NP\_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP\_h 6921333\_9; removed intron (146-893) predicted from blastx analysis.

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Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.T and H29974.

5 Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG\_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

10 The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was  
15 generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601\_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF  
20 was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG\_040010.

Human orthologue of AA671275\_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related  
25 kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

30 Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

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Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

5 The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase kinase 6 (MAP3K6) (NM\_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

10 The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

Prov. SEQ ID NO: (na)	Prov. SEQ ID NO: (aa)
160	196
213	214
215	216
122	126
119	123
148	184
4	20
7	23
205	206
14	30
15	31
35	56
42	63
51	72
44	65
77	91

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78	92
79	93
80	94
157	193

### Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR  
5 fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press  
10 (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNASTar). "DNA  
15 Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu, LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR  
20 fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press  
25 (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", "Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). "Kinase Domain Start", "Kinase Domain End", "Profile Start" and "Profile End" refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a "Profile Start" of 1 and a "Profile End" of 261. The boundaries of the catalytic domain within the overall protein are noted in the "Kinase Domain Start" and "Kinase Domain End" columns.

The following abbreviations were used for kinases:

ASK	Apoptosis signal-regulating kinase
CaMK	Ca <sup>2+</sup> /calmodulin-dependent protein kinase
CCRK	Cell cycle-related kinase
CDK	Cyclin-dependent kinase
CK	Casein kinase
DAPK	Death-associated protein kinase
DM	myotonic dystrophy kinase
Dyrk	dual-specificity-tyrosine phosphorylating-regulated kinase
GAK	Cyclin G-associated kinase
GRK	G-protein coupled receptor
GuC	Guanylate cyclase
HIPK	Homeodomain-interacting protein
IRAK	Interleukin-1 receptor-associated kin
MAPK	Mitogen activated protein kinase
MAST	Micotubule-associated STK
MLCK	Myosin-light chain kinase
MLK	Mixed lineage kinase
NIMA	NimA-related protein kinase
PKA	cAMP-dependent protein kinase
RSK	Ribosomal protein S6 kinase
RTK	Receptor tyrosine kinase



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SGK      Serum and glucocorticoid-regulated kinase  
STK      serine threonine kinase  
ULK      UNC-51-like kinase

The following abbreviations were used for species

H      Human  
M      Murine  
R      Rat  
FV      Fowlpox virus  
MT      *M. thermoautotrophicum*  
CE      *Caenorhabditis elegans*  
DM      *Drosophila melanogaster*  
OS      *Oryza sativa*  
SP      *Schizosaccharomyces pombe*  
TP      *Tetrahymena pyriformis*  
PI      *Petunia inflata*  
NC      *Neurospora crassa*  
MSV      *Medicago sativa*  
MSV      Moloney murine sarcoma virus  
SA      *Squalus acanthias*  
CS      *Cucumis sativus*  
GM      *Glycine max*  
LL      *Lilium longiflorum*  
TV      *Trichomonas vaginalis*  
MP      *Mycoplasma pneumoniae*  
DD      *Dictyostelium discoideum*  
SC      *Saccharomyces cerevisiae*  
MT      *Methanobacterium thermoautotrophicum*



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### Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program ([www.ch.embnet.org/software/COILS\\_form.html](http://www.ch.embnet.org/software/COILS_form.html)). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind ([www.at.embnet.org/embnet/tools/bio/PESTfind/](http://www.at.embnet.org/embnet/tools/bio/PESTfind/)). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, arginine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) *Science* 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging from about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

### **Identification of potential coiled-coil domains and PEST domains in N34132**

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coil-coil regions are shown below.

Table 11 coiled-coil domains predicted for N34132

Coiled-coil Region	Amino acid range	Length (aa)
1	124-147	24
2	437-451	15
3	495-526	32
4	1,723-1,749	27

5 Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

PEST Region	Score	Amino acid range	Amino Acid Length
1	+ 4.91	54-95	42
2	+11.4	537-570	34
3	+31.08	1293-1304	12
4	+10.15	1543-1565	23
5	+ 6.17	1698-1732	35

## 10 EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

### Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: <http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html>. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, <http://www.ncbi.nlm.nih.gov/Omim/searchomim.html>), The Genome Database (<http://gdb.infobiogen.fr/gdb/simpleSearch.html>), and the Whitehead Institute human physical map ([http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts\\_info?database=release](http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release)). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

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following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query against databases, such as dbsts and htgs (described at

5 [http://www.ncbi.nlm.nih.gov/BLAST/blast\\_databases.html](http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html)) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (<http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast>) and is used to query either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above,

10 Stanford University maintains a useful site for chromosomal mapping from STS data (<http://www-shgc.stanford.edu/RH/rhserverformnew.html>). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the

15 entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is also made using Medline

20 (<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

### Results

25 The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with

30 chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM)  
(<http://www.ncbi.nlm.nih.gov/htbin-post/Omim>).

### EXAMPLE 3: Generation of Specific Immunoreagents

#### Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNASTar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

Clone Name	SEQ ID NO (aa)	Peptide Sequence	Amino Location
AA8256850	124	KSRDNSRDSSQSEND	339-353
		TEKLKRSQDLPREPLP	372-386
		RGWRPYDIHS	223-232
5R79-46-1	126	FEGPRRNKEVMYK	224-236
		KDDYNETVHKKTE	451-463
		GTHPKDRNVEKLQ	541-553
		EVSKYQEYTNELQET	643-657
AA256100	129	IDDTSNFDDFPESDI	405-419
		TEPDYKSKDWVFL	427-439
		EEKKLRRSQHARKET	61-75
AA210825	130	SNKDTLRKRHYWRDL	507-521
		RHTTRKSSTTLRE	488-500
		FQNNTTNRYYYKEIPL	528-542
		GKHRKTGRDVAVK	668-680
		FPTKQESQLRNE	687-698

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AA316804	132	ESHVHQEPSKRIPS	239-252
		HTKRKSSTMVKEGW	409-422
		PSDLDERDEEAVK	375-388
		SPGQKGDHKLSTSI	543-557
R47805	143	EPVGRWDQDYDRAVL	44-58
		KPKGPGGKRGHKRLI	325-339
		PTDVAQLPSRVPRDA	219-233
AA234451	167	DPFDWEKTGNDGSLT	293-307
		HPRPQEKDVWEE	374-385
		RENTDEVFPDEQLSD	340-354
		RSEITQPDRDIPLVR	427-441
AA460132	180	LKSYSTSSKKARPVL	222-236
		KKLDEVRLRGRKRS	237-251
		ETEKTAQGLSNLAKT	131-145
N34132	183	SGRRRRPTKSKGSKS	1848-1862
		PGTAPSKPPLTKAPV	1474-1488
		VSDTQPKAPGIDD	1365-1378
		AHSLDKTSHSSTTGL	1253-1267
5R69-17-2	187	GTTREKTDRVKST	178-190
		HSEAPELHGKIRSSN	138-152
		DETVTPPQFSIV	87-98
		QYDVKSEIYS	204-213
AA278842	206	TVDPEKSVRDQAFKA	515-529
		DSSTADRWDDEDWGS	637-651
		SVSEDPTQLEEVK	539-553
AA836348	232	NAPTKRPRSSTVTEA	323-337
		LDSEEDYYTPQKVDV	514-528
		GDKASYRQPKHVEKL	409-423

#### EXAMPLE 4. Expression analysis of Novel Mammalian Protein Kinases

##### GENE EXPRESSION ANALYSIS

###### Tissue Arrays

"cDNA libraries" derived from a variety of sources were immobilized onto nylon membranes and probed with 32P-labeled cDNA fragments derived from the gene(s) of interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to generate single-stranded cDNAs (ss cDNA) that were tagged with specific sequences at each end. An oligo dT primer containing a specific sequence (CDS: AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when it adds additional C residues. If a primer (SMII: AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G: AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals to the added Cs and the MMLV recognizes the rest of the primer sequence as template and continues transcription. As a result, the synthesized cDNAs contain specific sequence tags at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same sequence (CDS and SMII) it is referred to as "symmetric." When the 5' end is tagged with a different sequence than the 3' end (CDS and ML2G) is referred to as "asymmetric." A double-stranded "cDNA library" is then generated by PCR amplification using the 3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2: AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified "cDNA libraries" were manually arrayed onto nylon membranes with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech) and hybridized with 32P labeled probes generated by random hexamer priming of cDNA fragments corresponding to the genes of interest. After washing, the blots were exposed to phosphorimaging cassettes and the intensity of the signal was quantified. The amount of the DNA on the arrays was also quantified by treating non-denatured or denatured arrays with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2 minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected



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with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

## 5 Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: "Tissue": tissue type of the cDNA; "Tumor sym", indicates that the tissue is derived from a tumor, "sym" refers to the fact that the 5' and 3' primers used to make the sample are the same; "Normal Sym", indicates normal tissue was used to make the sample, with symmetric primers as described above; "Tumor 1o", indicates that primary tumor tissue was used to make the cDNA; "Tumor cells", indicates that these cDNA samples were made from cultured tumor cells; "Normal", indicates that these samples are derived from normal tissue or cell lines; "Endos", indicates that these samples are derived from endothelium-related tissue sources; "p53" refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305176), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRJ), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AIG86865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

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EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

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Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

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EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Dbl and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

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Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.

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### CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush

group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

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What is claimed is:

CLAIMS

1. An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ  
5 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ  
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ  
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ  
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ  
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ  
10 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ  
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ  
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ  
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ  
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ  
15 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ  
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ  
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ  
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ  
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ  
20 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ  
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ  
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ  
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ  
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ  
25 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ  
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ  
ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ  
ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

(c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

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(d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(e) is the complement of the nucleotide sequence of (d);

(f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(g) is the complement of the nucleotide sequence of (f);

(h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID



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5 NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID  
NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID  
NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID  
NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID  
NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID  
NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID  
NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID  
NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID  
10 NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID  
NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID  
NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID  
NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID  
NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID  
NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID  
15 NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID  
NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID  
NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID  
NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID  
NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID  
20 NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID  
NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID  
NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID  
NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not  
all, of the domains selected from the group consisting of an N-terminal domain, a catalytic  
25 domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure  
region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or  
promoter effective to initiate transcription in a host cell.

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4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of  
5 SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126,  
SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131,  
SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,  
SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,  
10 SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,  
SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,  
SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,  
SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,  
SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,  
15 SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,  
SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,  
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,  
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,  
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
20 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,  
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,  
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,  
SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
25 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
30 and SEQ ID NO:242.

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7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, ~~SEQ ID NO:128~~, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

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9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

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11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ  
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ  
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ  
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ  
ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ  
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ  
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ  
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ  
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ  
ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ  
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ  
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ  
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ  
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ  
ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ  
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and  
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ  
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ  
ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ  
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ  
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ



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ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

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NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID  
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID  
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID  
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID  
5 NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID  
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID  
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID  
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID  
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID  
10 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID  
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID  
NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting  
of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a  
proline-rich region, a coiled-coil structure region, and a C-terminal tail.

15 13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated,  
purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a  
AA144574, AA116841, AA256100, AA305176, AA210825, AA316804, AA980090,  
20 N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515,  
AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215,  
AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936,  
W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838,  
25 W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a  
AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-  
1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859,  
30 AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a  
AA631990 or W08549 polypeptide.

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20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

5 22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836348, R86668 or N34132 polypeptide.

10 24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024 or SuRTK106 polypeptide.

15 25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.

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26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

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5 ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
10 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ  
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ  
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ  
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ  
15 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ  
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ  
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ  
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ  
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ  
20 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ  
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ  
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ  
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ  
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ  
25 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ  
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and  
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ  
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ  
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ  
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ  
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

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5 ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ  
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ  
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ  
ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ  
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ  
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ  
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ  
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ  
ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ  
10 ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ  
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ  
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ  
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ  
ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ  
15 ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and  
SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from  
the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a  
spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set  
20 forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID  
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID  
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID  
NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID  
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID  
25 NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID  
NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID  
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID  
NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID  
NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID  
30 NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID  
NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID  
NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

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NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID  
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID  
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID  
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID  
5 NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID  
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID  
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID  
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID  
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID  
10 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID  
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID  
NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting  
of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a  
proline-rich region, a coiled-coil structure region, and a C-terminal tail.

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28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,



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SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,  
SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,  
SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,  
SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,  
5 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,  
SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,  
SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,  
SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,  
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,  
10 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,  
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,  
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,  
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,  
15 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
20 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
and SEQ ID NO:242 with a test substance;

- (b) measuring the activity of said polypeptide; and
  - (c) determining whether said substance modulates the activity of said
- 25 polypeptide.

30. A method for identifying a substance that modulates kinase activity in a cell comprising:

- (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID
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5 NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID  
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID  
NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID  
NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID  
10 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID  
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID  
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID  
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID  
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID  
15 NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID  
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID  
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID  
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID  
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID  
20 NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID  
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID  
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID  
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID  
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID  
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID  
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

- (b) adding a test substance to said cell; and
- (c) monitoring a change in cell phenotype or the interaction between  
said polypeptide and a natural binding partner.

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31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.

34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) contacting said sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements of said sequences and fragments; and

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(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

- 5 (b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

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Table 1

Gene Name	SP	Prov	Seq ID	NA	Prov	Seq ID	AA	SEQ ID	ns	SEQ ID	ns	Family	Group	Length	NA	Length	AA	ORF	Start	ORF	End	ORF	Length	DNA Repeat	CHR Localization
X6117 h BAR2 h	H		1			1		122				AGC	GRK	2087	666			2084	1	2084		2084			22911
AA14374 m BAR2 m	M		17			2		123				AGC	GRK	1968	378			1964	2	1964		1964			NA
AA26859 h	H		140			3		124				AGC	MA3C11.1 ce	1788	418			1784	8	1784		1784		285-304	NA
AA98095 h	H		11			4		125				AGC	MA3C11.1 ce	3224	414			3220	65	3220		3220			1p18.1
5R7B-46 h TBK1 h	H		207			208		126				AGC	MA3C11.1 ce	3013	729			3009	93	3009		3009			NA
AA305176 h	H		42			9		127				AGC	NDR	1421	329			1417	53	1417		1417			10p11.2
AA116841 m	M		4			18		128				AGC	NDR	542	88			538	3	538		538			NA
AA256100 h	H		3			9		129				AGC	NDR	4683	164			4679	86	4679		4679			12q11
AA210825 h	H		5			21		130				AGC	PKC	3263	978			3259	117	3259		3259			18q13-q13.3
AA127269 h	H		203			204		131				AGC	PKC	315	105			311	1	311		311			NA
AA316804 h EPK2	H		6			22		132				AGC	PKC	2673	890			2669	1	2669		2669			22q12.2
AA2050 h PKNbeta	H		8			24		133				AGC	PKC	2670	889			2666	1	2666		2666			NA
AA21023 m PKNbeta	M		x			x		134				AGC	PKC	978	205			974	2	974		974			5p9.3
AA1702 h	H		12			28		135				AGC	SKK	1155	364			1151	1	1151		1151			12q12-q13.1
AA175653 h RPS8/C1	H		8			25		136				AGC	SKK	1410	468			1406	1	1406		1406			Xq21.1
AA215980 h	H		10			28		137				AGC	SKK	2738	745			2734	1	2734		2734			14q24.3
SGK h	H		227			228		138				AGC	SKK	1850	549			1846	1	1846		1846			8p21-q22
AA107515 m	M		x			x		139				AGC	SKK	1398	431			1394	1	1394		1394			18q13-q13.3
AA107515 m	M		x			x		140				AGC	SKK	2132	430			2128	25	2128		2128			NA
AA109508 m	M		13			29		141				AGC	SKK	1346	244			1342	2	1342		1342			NA
AA887783 h SGK1 SGK2	H		16			32		142				AGC	SKK	2260	446			2256	36	2256		2256			NA
AA17805 h PTNBL	H		33			54		143				AGC	SKK	1050	349			1046	1	1046		1046			3p14.3
AA20215 h	H		11			33		144				AGC	SKK	2310	440			2306	420	2306		2306			1p31.1-p32.3
SGK324 h	H		x			x		145				AGC	SKK	3240	692			3236	7	3236		3236			NA
AA20248 m SGK324 m	M		38			57		146				AGC	SKK	1248	297			1244	1	1244		1244			NA
AA20248 m SGK324 m	M		38			57		147				AGC	SKK	2474	668			2470	1	2470		2470			NA
AA20248 m SGK324 m	M		38			57		148				AGC	SKK	2474	668			2470	1	2470		2470			NA
AA197883 h	H		34			55		149				AGC	SKK	2474	668			2470	1	2470		2470			NA
AA172300 h DRK2	H		37			58		150				AGC	SKK	1638	373			1634	282	1634		1634			2p21.2
AA172300 h DRK2	H		37			58		151				AGC	SKK	2871	372			2867	171	2867		2867			NA
AA172300 h DRK2	H		37			58		152				AGC	SKK	1245	414			1241	1	1241		1241			NA
AA172300 h DRK2	H		37			58		153				AGC	SKK	4231	1311			4227	148	4227		4227			NA
AA172300 h DRK2	H		37			58		154				AGC	SKK	2311	438			2307	871	2307		2307			NA
AA172300 h DRK2	H		37			58		155				AGC	SKK	2190	779			2186	1	2186		2186			NA
AA172300 h DRK2	H		37			58		156				AGC	SKK	1584	520			1580	1	1580		1580			NA
AA172300 h DRK2	H		37			58		157				AGC	SKK	1330	230			1326	77	1326		1326			NA
AA172300 h DRK2	H		37			58		158				AGC	SKK	5183	928			5179	155	5179		5179			NA
AA172300 h DRK2	H		37			58		159				AGC	SKK	2291	629			2287	103	2287		2287			NA
AA172300 h DRK2	H		37			58		160				AGC	SKK	2145	714			2141	1	2141		2141			NA
AA172300 h DRK2	H		37			58		161				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		162				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		163				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		164				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		165				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		166				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		167				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		168				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		169				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		170				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		171				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		172				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		173				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		174				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		175				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		176				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		177				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		178				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		179				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		180				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		181				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		182				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		183				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		184				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		185				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		186				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		187				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		188				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		189				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		190				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		191				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58		192				AGC	SKK	2628	871			2624	1	2624		2624			NA
AA172300 h DRK2	H		37			58																			

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Table 1 (cont'd)

Gene Name	SP	Prov	Seq	ID	NA	Prov	Seq	ID	AA	SEQ	ID	NA	SEQ	ID	NA	Group	Length	NA	Length	AA	ORF	Start	ORF	End	ORF	Length	DNA Repeats	CHR Localization
BCON3 h	H															Other	184	84	184	184	113	113	1717	1717	1608	240-287	NA	
AA2711028 m	M															Other	185	85	184	184	113	113	1717	1717	1608	240-287	NA	
AA009102 h CAUKK	H															Other	186	86	186	186	114	114	1764	1764	1724	65-84	1203-314	
SR60 17.2 h	H															Other	187	87	187	187	115	115	2572	2572	723	406-521	NA	
H05011 h	H															Other	188	88	188	188	116	116	3895	3895	3513	1328-1348	CHR7	
AA02103 h DYRK3	H															Other	189	89	189	189	117	117	1911	1911	1859	3	NA	
AA589241 m DYRK3 m	M															Other	190	90	190	190	118	118	504	504	504	3	NA	
5R72 16.2 h R19027 h	H															Other	191	91	191	191	119	119	4968	4947	3	3	NA	
R43524 h, HRI h, R19009	H															Other	192	92	192	192	120	120	1890	1890	1890	2285-2365	NA	
17000057519457 h	H															Other	193	93	193	193	121	121	977	977	759	3	NA	
AA013324 m	M															Other	194	94	194	194	122	122	648	648	648	3	NA	
1700013901107 h, IRAK4	H															Other	195	95	195	195	123	123	1768	1768	1768	3	NA	
AA040508 m, IRAK4 m	M															Other	196	96	196	196	124	124	1173	1173	1176	3	NA	
AA085412 h	H															Other	197	97	197	197	125	125	2786	2786	2786	3	NA	
HGP 6644466	H															Other	198	98	198	198	126	126	1144	1144	966	3	NA	
AA449547 m	M															Other	199	99	199	199	127	127	841	840	840	602-621	NA	
SR57 10.2 m TESK2 m	M															Other	200	100	200	200	128	128	124	123	123	3	NA	
AA232253 h	H															Other	201	101	201	201	129	129	2400	2400	2400	3	NA	
A1375137 h	H															Other	202	102	202	202	130	130	2595	2595	2595	2210-2218	NA	
H97065 h	H															Other	203	103	203	203	131	131	2092	2092	1602	834	131	
W20810 m	M															Other	204	104	204	204	132	132	890	890	890	3	NA	
AA744236 h	H															Other	205	105	205	205	133	133	2094	2094	2094	3	NA	
A0527250 h	H															Other	206	106	206	206	134	134	1888	1888	1515	1515	1323	
AA378842 h	H															Other	207	107	207	207	135	135	1949	1949	1949	3	NA	
AA509388 h	H															Other	208	108	208	208	136	136	1599	1599	1599	3	NA	
AA429725 h	H															Other	209	109	209	209	137	137	987	987	987	3	NA	
SGK022 h	H															Other	210	110	210	210	138	138	1004	1004	804	3	NA	
AA060026 m SGK022 m	M															Other	211	111	211	211	139	139	372	372	1244	878	1461-1411	
AA399069 h	H															Other	212	112	212	212	140	140	101	101	1174	1074	3	NA
AA756539 h	H															Other	213	113	213	213	141	141	819	819	819	3	NA	
AA833975 h	H															Other	214	114	214	214	142	142	385	385	1012	648	3	NA
AA905446 h	H															Other	215	115	215	215	143	143	2	2	1000	968	3	NA
H26974 h	H															Other	216	116	216	216	144	144	1236	1236	1032	3	NA	
AA408104 m H26974 m	M															Other	217	117	217	217	145	145	1221	1221	1032	3	NA	
AA215311 h	H															Other	218	118	218	218	146	146	1555	1555	1443	3	NA	
AA019361 h	H															Other	219	119	219	219	147	147	1835	1835	1885	3	NA	
AA311714 h	H															Other	220	120	220	220	148	148	117	117	117	39	NA	
SGK384 h	H															Other	221	121	221	221	149	149	222	222	1268	225-1228	NA	
AA210451 m SGK384 m	M															Other	222	122	222	222	150	150	2112	2112	2112	57-76, 318-337	NA	
SGK071.2 h	H															Other	223	123	223	223	151	151	1820	1820	1820	3	NA	
019653.9 h	H															Other	224	124	224	224	152	152	1820	1820	1820	240-259	NA	
AA306001 m	M															Other	225	125	225	225	153	153	1087	1086	1086	3	NA	
AA481275 h VRK3	H															Other	226	126	226	226	154	154	1422	1422	1422	3	NA	
ST1575 m VRK3 m	M															Other	227	127	227	227	155	155	704	704	704	3	NA	
AA452847 h MPCK1	H															Other	228	128	228	228	156	156	915	915	915	3	NA	
H05721 h	H															Other	229	129	229	229	157	157	1937	1937	1743	3	NA	
A08B865 h	H															Other	230	130	230	230	158	158	2508	2508	2508	3	NA	
AA430346 h	H															Other	231	131	231	231	159	159	3033	3033	3033	3	NA	
RR6668 h MCK6	H															Other	232	132	232	232	160	160	1485	1485	1485	3	NA	
PAK6 h S905-20-11	H															Other	233	133	233	233	161	161	2157	2157	2157	3	NA	
SRRT100 h 2R41-9-4 h	H															Other	234	134	234	234	162	162	1465	1465	1465	3	NA	
AA098024 m	M															Other	235	135	235	235	163	163	549	549	549	3	NA	
SGK2a96a h	H															Other	236	136	236	236	164	164	1358	1358	1358	3	NA	
H0950 h CCRK	H															Other	237	137	237	237	165	165	1358	1358	1358	3	NA	
MM 007170 h TESK2	M															Other	238	138	238	238	166	166	2060	2060	2060	3	NA	
AA007170 h	H															Other	239	139	239	239	167	167	1885	1885	1885	3	NA	



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Table 2

SP	Seq ID#	Patent	Seq ID#	Family	Group	nraa Pscore	Length aa	ID match aa	% Identity	% Similar	nraa Match ACC#	Description	Kinase Domain(s) start	Kinase Domain(s) end	Profile start	Profile end
H	1	122	AGC	GRK	GRK	2.7e-314	888	887	100	100	CAB45637.1	BAR2 [Homo sapiens]	191	453	1	261
H	2	123	AGC	GRK	GRK	1.30E-190	378	371	98	99	NP_037029.1	Adrenoreceptor kinase, beta 2 (G-protein-linked receptor kinase)	3	143	121	261
H	3	124	AGC	GRK	GRK	5.80E-108	419	262	71	86	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	28	286	1	261
H	4	125	AGC	GRK	GRK	1.40E-137	414	414	100	100	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	23	283	1	261
H	5	126	AGC	GRK	GRK	1.40E-137	414	414	100	100	NP_037386.1	TANK-binding kinase 1 [Homo sapiens]	9	304	1	261
H	6	127	AGC	GRK	GRK	1.20E-09	329	73	46	66	BAA76817.1	KIAA0973 protein [Homo sapiens]	35	310	1	261
H	7	128	AGC	GRK	GRK	1.30E-19	86	42	49	71	AAF55594.1	CG719 gene product [Drosophila melanogaster]	24	44	242	261
H	8	128	AGC	GRK	GRK	6.10E-181	464	463	100	100	BAA76809.1	KIAA0965 protein [Homo sapiens]	90	383	1	261
H	9	130	AGC	GRK	GRK	8.80E-160	978	815	87	80	NP_007333.1	Protein kinase C, mu [Homo sapiens]	651	907	1	261
H	10	131	AGC	GRK	GRK	1.10E-10	105	42	42	57	P05127	Protein kinase C, beta-11 TYPE (PKC-BETA-2) [Homo sapiens]	19	24	256	261
H	11	132	AGC	GRK	GRK	0	880	890	100	100	NP_005804.1	Protein kinase C, nu [Homo sapiens]	578	832	1	261
H	12	133	AGC	GRK	GRK	9.4e-319	889	889	100	100	NP_037487.1	PKNbeta [Homo sapiens]	559	818	1	261
H	13	134	AGC	GRK	GRK	1.20E-108	205	204	100	100	JC7083	Protein kinase N beta [Homo sapiens]	1	134	126	261
H	14	135	AGC	GRK	GRK	3.60E-12	384	94	38	55	AAC82495.1	Ribosomal protein S6 kinase 3 [Homo sapiens]	81	333	1	261
H	15	136	AGC	GRK	GRK	2.90E-257	469	469	100	100	NP_038556.1	Ribosomal protein S6 kinase 3 [Homo sapiens]	225	459	1	261
H	16	137	AGC	GRK	GRK	7.00E-178	745	745	100	100	NP_055311.1	Ribosomal protein S6 kinase, 90KD, polypeptide 6 [Homo sapiens]	73 & 428	330 & 683	1	261
H	17	138	AGC	GRK	GRK	9.80E-222	549	549	100	100	AAD30182.1	Unknown [Homo sapiens]	153	539	1	261
H	18	139	AGC	GRK	GRK	9.20E-103	431	430	100	100	AAD41091.1	SGK [Homo sapiens]	98	355	1	261
H	19	140	AGC	GRK	GRK	2.80E-157	430	429	99	98	NP_035491.1	Serum/glucocorticoid regulated kinase [Mus musculus]	98	354	1	261
H	20	141	AGC	GRK	GRK	2.00E-78	244	244	100	100	AAF12757.2	Protein kinase [Homo sapiens]	162	369	1	261
H	21	142	AGC	GRK	GRK	4.10E-211	446	375	88	88	AAF27051.1	SGK-like protein SGK [Homo sapiens]	10	17	253	261
H	22	143	AGC	GRK	GRK	5.80E-216	349	349	100	100	NP_009215.1	Protein kinase [Homo sapiens]	40	333	1	261
H	23	144	AGC	GRK	GRK	1.40E-19	440	38	39	61	CAA04119.1	Phosphoprotein [Homo sapiens]	388	625	1	261
H	24	145	AGC	GRK	GRK	1.50E-165	699	466	65	77	O15075	DCAMKL1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1)	59	297	1	261
H	25	146	AGC	GRK	GRK	1.60E-62	297	199	67	83	AAF26875.1	CPG16 [Mus musculus]	415	673	1	261
H	26	147	AGC	GRK	GRK	2.60E-48	708	181	44	60	O15075	CPG16 [Mus musculus]	514	771	1	261
H	27	148	AGC	GRK	GRK	2.60E-31	806	147	55	73	AAF26875.1	CPG16 [Mus musculus]	33	293	1	261
H	28	149	AGC	GRK	GRK	3.10E-121	372	372	100	100	NP_004217.1	Death-associated protein kinase-related 2	32	293	1	261
H	29	150	AGC	GRK	GRK	7.90E-93	372	340	91	95	NP_004217.1	Death-associated protein kinase-related 2	32	293	1	261
H	30	151	AGC	GRK	GRK	1.20E-113	414	414	100	100	NP_004751.1	Death-associated protein kinase-related 1	8	259	1	261
H	31	152	AGC	GRK	GRK	5.80E-165	1311	1053	80	80	BAA76843.1	KIAA0999 protein [Homo sapiens]	74	325	1	261
H	32	153	AGC	GRK	GRK	1.20E-45	438	153	51	70	T22427	Hypothetical protein F49C5.4 - [Caenorhabditis elegans]	415	673	1	261
H	33	153	AGC	GRK	GRK	1.40E-32	438	122	46	65	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	58	307	1	261
H	34	154	AGC	GRK	GRK	1.30E-184	729	729	100	100	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	58	307	1	261
H	35	155	AGC	GRK	GRK	3.50E-128	462	462	100	100	AAC33487.1	R31237, partial CDS [Homo sapiens]	59	340	1	261
H	36	156	AGC	GRK	GRK	0	1330	1235	100	100	BAA09484.1	KIAA0135 gene is related to pim-1 oncogene, [Homo sapiens]	999	1258	1	261
H	37	157	AGC	GRK	GRK	5.10E-59	230	183	79	85	BAA09484.1	KIAA0135 gene is related to pim-1 oncogene, [Homo sapiens]	1	158	23	261
H	38	158	AGC	GRK	GRK	3.00E-111	926	636	100	100	BAA34501.1	KIAA0781 protein [Homo sapiens]	20	271	1	261
H	39	159	AGC	GRK	GRK	7.30E-80	629	387	57	89	NP_055655.1	KIAA0537 gene product [Homo sapiens]	53	304	1	261
H	40	160	AGC	GRK	GRK	1.40E-244	714	714	100	100	NP_055401.1	Homomally upregulated neu tumor-associated kinase [Homo sapiens]	81	320	1	261
H	41	161	AGC	GRK	GRK	8.20E-76	874	211	63	80	AAAT3168.1	Skeletal muscle myosin light chain kinase [Gallus gallus]	570	825	1	261
H	42	162	AGC	GRK	GRK	0	2288	2227	100	100	BAA92535.1	KIAA1297 protein [Homo sapiens]	820 & 1068	873 & 1358	1	261
H	43	163	AGC	GRK	GRK	7.80E-37	127	67	99	99	BAA92535.1	KIAA1297 protein [Homo sapiens]	3	76	186	261
H	44	164	AGC	GRK	GRK	0	1287	1284	100	100	NP_008955.1	STK with Dbr- and pleckstrin homology domains [Homo sapiens]	985	1239	1	261
H	45	165	AGC	GRK	GRK	5.00E-20	514	114	41	63	P25223	MLCK [Dictyostelium discoideum]	116	381	1	261
H	46	166	AGC	GRK	GRK	3.30E-89	508	181	53	85	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	34	313	1	261
H	47	167	AGC	GRK	GRK	8.80E-98	478	188	57	88	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	21	471	1	261
H	48	168	AGC	GRK	GRK	9.60E-39	286	138	82	79	NP_038527.1	PFTAIRE protein kinase 1 [Homo sapiens]	1	218	23	261
H	49	169	AGC	GRK	GRK	7.10E-48	247	146	59	75	NP_004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	191	23	261

Table 2 (cont'd)

M	50	170	CMGC	CDK	2,90E-84	286	193	65	78	NP 004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	240	24	261
M	51	171	CMGC	CDK	1.10E-204	1490	1490	100	100	AAF36401.1	GDC2-related protein kinase 7 [Homo sapiens]	21	1020	1	261
H	52	172	CMGC	CDK	9.20E-101	534	377	82	82	AAF36509.1	NKIATRE [Homo sapiens]	4	365	1	261
M	53	173	CMGC	CDK	1.40E-128	337	225	92	96	AAF34871.1	NKIATRE alpha [Rattus norvegicus]	1	28	235	261
M	54	174	CMGC	CDK	3.00E-68	211	159	79	84	NP 036251.1	Cell cycle related kinase [Homo sapiens]	1	153	134	261
M	55	175	CMGC	CLK	1.50E-242	499	436	91	93	NP 031740.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	177	493	1	261
H	56	176	CMGC	RCK	9.10E-89	544	343	57	64	AAD12719.1	Extracellular signal-regulated kinase 7, ERK7 [Rattus norvegicus]	13	305	1	261
H	57	177	CMGC	RCK	2.30E-189	419	419	100	100	NP 055041.1	Renal tumor antigen [Homo sapiens]	4	285	1	261
M	58	178	CMGC	RCK	1.50E-180	632	632	100	100	AAF37278.1	Intestinal cell kinase [Homo sapiens]	4	284	1	261
M	59	179	CMGC	RCK	1.80E-79	413	198	60	77	P20689	MLCK [Rattus norvegicus]	109	364	1	261
H	60	180	Microbial PK	YGR262.sc	2.50E-45	253	102	46	67	AAF50799.1	CG10673 gene product [Drosophila melanogaster]	101	187	65	147
H	61	181	Other	C28C2.ce	2.30E-158	509	258	100	100	CAB70864.1	Hypothetical protein [Homo sapiens]	2	267	1	261
M	62	182	Other	C28C2.ce	1.80E-152	281	243	94	98	CAB70864.1	Hypothetical protein [Homo sapiens]	59	86	235	261
H	63	183	Other	C28C2.ce	6.70E-300	1952	1193	99	99	NP 055638.1	KIAA0344 gene product [Homo sapiens]	221	479	1	261
H	64	184	Other	C28C2.ce	1.10E-254	535	535	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	73	327	1	261
M	65	185	Other	C28C2.ce	2.50E-208	378	372	98	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	170	85	261
M	66	186	Other	CAMKK	3.80E-148	588	588	100	100	AAO31507.1	Ca2+/calmodulin-dependent protein kinase beta [Homo sapiens]	165	446	1	261
H	67	187	Other	CTRI	9.90E-24	287	87	33	52	JQ1743	Hypothetical 33.6K protein - rabbit fibroblast virus	24	285	1	261
H	68	188	Other	DYRK	0	1171	1137	97	99	AAO52566.1	Nuclear body associated kinase 1a [Mus musculus]	199	527	1	261
H	69	189	Other	DYRK	2.10E-280	553	553	100	100	NP 003573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	174	487	1	261
M	70	190	Other	DYRK	2.30E-95	188	149	90	96	NP 003573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	174	487	1	261
H	71	191	Other	EIFK	0	1649	1493	90	96	NP 038747.1	GCN2 eIF2alpha kinase [Mus musculus]	76	103	235	261
H	72	192	Other	EIFK	1.50E-220	630	630	100	100	NP 055228.1	Heme-regulated initiation factor 2 alpha kinase [Homo sapiens]	167	583	1	261
H	73	193	Other	Endop	2.50E-45	253	102	46	67	AAF50799.1	CG10673 gene product [Drosophila melanogaster]	101	187	65	147
M	74	194	Other	Endop	3.70E-45	216	100	45	64	AAF50799.1	(AE003567) CG10673 gene product [Drosophila melanogaster]	116	150	116	147
M	75	195	Other	IRAK	0	596	596	100	100	NP 009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	165	443	1	261
M	76	196	Other	IRAK	1.20E-170	392	293	75	85	NP 009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	516	777	1	261
H	77	197	Other	IRE	1.5e-323	922	746	82	88	NP 036146.1	Ira1, inositol-requiring 1 gene [Mus musculus]	32	318	1	261
H	78	198	Other	KYK2.dd	8.70E-40	225	102	45	62	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	12	266	1	261
H	79	199	Other	KYK2.dd	5.90E-32	280	109	32	50	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	12	39	101	128
M	80	200	Other	LMK	2.80E-17	41	37	92	95	NP 009101.1	Testis-specific kinase 2 [Homo sapiens]	16	259	1	261
M	81	201	Other	MLK	2.50E-282	800	799	100	100	AAF63490.1	Mixed lineage kinase [Homo sapiens]	463	723	1	261
H	82	202	Other	MLK	8.80E-251	835	835	100	100	AAF63490.1	Mixed lineage kinase [Homo sapiens]	357	620	1	261
H	83	203	Other	RIP	2.20E-158	634	365	100	100	BA043217.1	Pulative protein-tyrosine kinase [Homo sapiens]	7	27	181	202
M	84	204	Other	RIP	5.30E-158	289	288	100	100	AAF03133.1	Receptor interacting protein 3 [Mus musculus]	57	83	50	78
M	85	205	Other	SCY1.sc	0	688	688	100	100	CAB55300.1	Hypothetical protein [Homo sapiens]	32	327	1	261
H	86	206	Other	SCY1.sc	1.70E-209	505	354	98	98	BA042598.1	KIAA1360 protein [Homo sapiens]	65	131	47	116
H	87	207	Other	SCY1.sc	2.20E-157	808	398	45	61	AAF56933.1	CG1973 gene product [Drosophila melanogaster]	230	305	81	143
H	88	208	Other	SLOB7	7.40E-196	649	649	100	100	BA091097.1	Unnamed protein product [Homo sapiens]	79	531	1	261
H	89	209	Other	SRPK	5.80E-252	533	533	100	100	NP 055185.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	10	265	1	261
H	90	210	Other	STK22A	3.80E-53	268	122	46	70	NP 033461.1	Serine/threonine kinase 22B (spemogenesis associated)	25	260	1	261
M	91	211	Other	STK22	2.70E-52	268	127	48	68	NP 033461.1	Serine/threonine kinase 22A (spemogenesis associated)	12	272	1	261
H	92	212	Other	STK22A	4.60E-16	292	112	45	64	NP 033461.1	Serine/threonine kinase 22B (spemogenesis associated)	12	267	1	261
H	93	213	Other	STK22A	5.10E-123	358	322	90	96	NP 033461.1	Serine/threonine kinase 22B (spemogenesis associated)	1	213	7	261
H	94	214	Other	TSK	2.10E-33	273	122	46	62	NP 033461.1	Serine/threonine kinase 22B (spemogenesis associated)	1	329	1	261
H	95	215	Other	TSK	2.50E-32	216	93	41	58	NP 033461.1	Serine/threonine kinase 22B (spemogenesis associated)	80	408	1	261
H	96	216	Other	UNC	0.000082	333	57	36	56	AAO32787.1	Pulative protein kinase [Arabidopsis thaliana]	8	340	1	261
M	97	217	Other	UNC	0.002492	412	53	37	52	BA077341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	57	313	1	261
M	98	218	Other	UNC	0.001096	341	50	36	56	BA077341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	57	313	1	261
H	99	219	Other	UNC	1.90E-68	480	247	100	100	T17285	Hypothetical protein DKF434C131.1 - human (fragment)	4	285	1	261
H	100	220	Other	UNC	1.60E-208	565	468	96	96	BA091270.1	Unnamed protein product [Homo sapiens]	1	39	84	124
H	101	221	Other	UNC	1.60E-208	565	468	96	96	BA091270.1	Unnamed protein product [Homo sapiens]	1	39	84	124
H	102	221	Other	Unique	8.70E-10	39	27	69	90	AAO05575.1	Serum-inducible kinase [Homo sapiens]	1	39	84	124

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Table 2 (cont'd)

M	103	222	Other	Unique	0.000022	349	38	30	50	CAA18116.1	Serine/threonine protein kinase like protein [Arabidopsis thaliana]	80	159	1	88
H	104	223	Other	Unique	0.000126	704	54	30	45	BAA86578.1	KIAA1284 protein [Homo sapiens]	1	246	25	261
M	105	224	Other	Unique	0.000385	540	25	42	61	AAF47916.1	Tle gene product [Drosophila melanogaster]	9	104	168	261
H	106	225	Other	Unique	0.31334	540	52	30	42	P10162	SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [Homo sapiens]	1	272	18	73
M	107	226	Other	Unique	0.022848	365	25	34	57	NP_000276.1	Testis-specific kinase 1 [Homo sapiens]	68	96	42	71
H	108	227	Other	VRK	3.10E-263	474	474	100	100	BAA90769.1	Vaccinia related kinase 3 [Homo sapiens]	247	318	63	136
M	109	228	Other	VRK	1.20E-111	234	191	82	90	BAA90769.1	Vaccinia related kinase 3 [Homo sapiens]	7	78	83	136
H	110	229	Other	YPL236.sc	7.40E-144	305	304	100	100	AAC28337.1	MPSK [Homo sapiens]	20	290	1	261
H	111	230	Other	YQ09.c6	5.10E-49	581	135	43	83	AAF46188.1	CG4523 gene product [Drosophila melanogaster]	156	507	1	261
H	112	231	STE	NEK	3.30E-30	898	122	48	67	P51954	NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus]	4	251	1	261
H	113	232	STE	NEK	2.70E-119	838	357	88	86	AAD31939.1	(AC007055) unknown [Homo sapiens]	52	308	1	261
H	114	233	STE	STE11	1.10E-291	1011	1011	100	100	NP_004683.1	mitogen-activated protein kinase kinase kinase 8 [Homo sapiens]	376	629	6	261
H	115	234	STE	STE20-02	7.70E-177	719	719	100	100	BAA94194.1	(AB040812) protein kinase PAK5 [Homo sapiens]	449	700	1	261
M	116	235	TK	RTK-20	4.90E-24	495	77	38	56	AAA98465.1	(U00827) protein tyrosine kinase [Mus musculus]	187	453	1	261
H	117	236	TK	RTK-20	5.30E-18	183	53	38	57	NP_032036.1	fibroblast growth factor receptor 3 [Mus musculus]	8	143	123	261
H	118	237	AGC	SGK	6.30E-112	367	367	100	100	AAF12757.2	SGK2alpha protein kinase [Homo sapiens]	35	292	1	261
H	120	238	CMGC	CDK	2.80E-137	452	452	100	100	NP_036251.1	Cell cycle related kinase [Homo sapiens]	4	267	1	261
H	121	239	Other	LMK	6.50E-233	555	555	100	100	NP_009101.1	Testis-specific kinase 2 [Homo sapiens]	62	293	5	261

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Table 3

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Tissue	Tumor type	Normal type	Tumor - to	Tumor cells	Normal	Endom	p33	SEQ 003	AREG	5	TMH	SEQ 004	AREG	304	AREG	3	CAESG	11	EMSG	12	PMSE	14	NHSG	16	18
adrenal gland - h	1	1						7490	10611	50122		29481	34705	56981	11808	16820	12165								
adrenal node - h	2	2						8151	12255	1202494	118257	105718	55339	19907	94529	12509									
adrenal node - h	3	3						4485	9226	1477586	35387	32227	33560	13151	20224	12509									
adrenal node - h	4	4						964	378	109897		4021	4318	1984	1985	24739	7907								
adrenal node - h	5	5						9649	5023	236783	62822	21880	7861	7736	34253	2103									
adrenal node - h	6	6						5423	3574	334665	50825	32200	8621	11808	12509	12509									
adrenal node - h	7	7						6350	19704	787233	64608	35692	16370	28260	62536	12509									
adrenal node - h	8	8						8342	7884	175184	82472	34569	18473	11010	87365	12186									
adrenal node - h	9	9						15719	6044	967041	86401	30156	23343	13781	103271	8901									
adrenal node - h	10	10						8763	15456	123178	46305	43070	24271	13881	82242	10901									
adrenal node - h	11	11						4107	10639	337527	51069	47948	31171	19908	65084	10889									
adrenal node - h	12	12						3477	1784	122056	82262	59484	31891	11790	8484	74734	11184								
adrenal node - h	13	13						3307	5284	1584113	28106	35129	17029	10418	88677	14403									
adrenal node - h	14	14						2725	3608	429781	37947	37750	11433	34594	82518	15635									
adrenal node - h	15	15						8315	6481	1305467	79674	12519	10848	11874	57631	8205									
adrenal node - h	16	16						5463	5185	187682	81053	12519	10848	11874	57631	8205									
adrenal node - h	17	17						3020	1915	227834	27478	20673	6357	11717	42378	11051									
adrenal node - h	18	18						3568	5455	412001	41491	21502	7820	8806	48325	12082									
adrenal node - h	19	19						5186	2788	224006	21086	12272	12286	4848	54755	8788									
adrenal node - h	20	20						3182	4479	303847	34683	16281	16556	6363	40333	8303									
adrenal node - h	21	21						3364	1518	208605	48111	29973	10030	4418	37827	7084									
adrenal node - h	22	22						4121	1821	448637	251205	26471	9670	3699	18010	5109									
adrenal node - h	23	23						4121	1821	448637	251205	26471	9670	3699	18010	5109									
adrenal node - h	24	24						6542	15363	1255993	90041	19148	11793	29138	83525	13780									
adrenal node - h	25	25						7658	4906	1814062	122488	62448	45509	21130	83525	13780									
adrenal node - h	26	26						7204	0	0	0	0	0	0	0	0									
adrenal node - h	27	27						7204	0	0	0	0	0	0	0	0									
adrenal node - h	28	28						7204	0	0	0	0	0	0	0	0									
adrenal node - h	29	29						24571	1970	10230	42836	25961	86271	9143	43670	7164									
adrenal node - h	30	30						8724	3099	857793	60488	24824	15301	4715	11713	65164	2638								
adrenal node - h	31	31						7791	1356	128866	24824	15301	4715	11713	65164	2638									
adrenal node - h	32	32						3364	4849	34257	34433	33331	14725	15085	11717	8203									
adrenal node - h	33	33						7876	0	0	0	0	0	0	0	0									
adrenal node - h	34	34						11688	519	41843	15418	16140	8140	6513	44443	7564									
adrenal node - h	35	35						8132	721	47839	15781	20735	8420	8512	44078	7285									
adrenal node - h	36	36						3364	1518	208605	48111	29973	10030	4418	37827	7084									
adrenal node - h	37	37						8890	2171	148493	16335	13506	5418	2447	30471	8104									
adrenal node - h	38	38						7091	745	50119	15263	3652	2515	3620	47872	7275									
adrenal node - h	39	39						3710	2472	87220	40813	17473	10184	1802	70722	11800									
adrenal node - h	40	40						2879	0	0	0	0	0	0	0	0									
adrenal node - h	41	41						12386	3565	21478	20965	16311	15615	3562	40860	8373									
adrenal node - h	42	42						4458	0	0	0	0	0	0	0	0									
adrenal node - h	43	43						8962	23889	33514	19562	14956	19562	19562	19562	19562									
adrenal node - h	44	44						115	257	9191	3386	2181	144	1080	8245	803									
adrenal node - h	45	45						0	0	0	0	0	0	0	0	0									
adrenal node - h	46	46						0	0	0	0	0	0	0	0	0									
adrenal node - h	47	47						0	0	0	0	0	0	0	0	0									
adrenal node - h	48	48						0	0	0	0	0	0	0	0	0									
adrenal node - h	49	49						0	0	0	0	0	0	0	0	0									
adrenal node - h	50	50						0	0	0	0	0	0	0	0	0									
adrenal node - h	51	51						0	0	0	0	0	0	0	0	0									
adrenal node - h	52	52						0	0	0	0	0	0	0	0	0									
adrenal node - h	53	53						0	0	0	0	0	0	0	0	0									
adrenal node - h	54	54						0	0	0	0	0	0	0	0	0									
adrenal node - h	55	55						0	0	0	0	0	0	0	0	0									
adrenal node - h	56	56						0	0	0	0	0	0	0	0	0									
adrenal node - h	57	57						0	0	0	0	0	0	0	0	0									
adrenal node - h	58	58						0	0	0	0	0	0	0	0	0									
adrenal node - h	59	59						0	0	0	0	0	0	0	0	0									
adrenal node - h	60	60						0	0	0	0	0	0	0	0	0									
adrenal node - h	61	61						0	0	0	0	0	0	0	0	0									
adrenal node - h	62	62						0	0	0	0	0	0	0	0	0									
adrenal node - h	63	63						0	0	0	0	0	0	0	0	0									
adrenal node - h	64	64						0	0	0	0	0	0	0	0	0									
adrenal node - h	65	65						0	0	0	0	0	0	0	0	0									
adrenal node - h	66	66						0	0	0	0	0	0	0	0	0									
adrenal node - h	67	67						0	0	0	0	0	0	0	0	0									
adrenal node - h	68	68						0	0	0	0	0	0	0	0	0									
adrenal node - h	69	69						0	0	0	0	0	0	0	0	0									
adrenal node - h	70	70						0	0	0	0	0	0	0	0	0									
adrenal node - h	71	71						0	0	0	0	0	0	0	0	0									
adrenal node - h	72	72						0	0	0	0	0	0	0	0	0									
adrenal node - h	73	73						0	0	0	0	0	0	0	0	0									
adrenal node - h	74	74						0	0	0	0	0	0	0	0	0									
adrenal node - h	75	75						0	0	0	0	0	0	0	0	0									
adrenal node - h	76	76						0	0	0	0	0	0	0	0	0									
adrenal node - h	77	77						0																	

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Table 3 (cont'd)

Tissue	Termen - yz	Marin - yz	Termen - 1a	1a - 2a	2a - 3a	3a - 4a	4a - 5a	5a - 6a	6a - 7a	7a - 8a	8a - 9a	9a - 10a	10a - 11a	11a - 12a	12a - 13a	13a - 14a	14a - 15a	15a - 16a
Ha 5787	155							120711	0	189524	349411	18731	12712	80761	48623	5914		
MCF-7/ADRI-RES	153							132420	1272	212001	252021	8771	1787	86701	48543	5188		
MCF-7	151							18337	1099	630667	62618	21779	15800	10732	33949	5115		
LUCC-7	145							5452	568	304414	11714	10734	16348	2264	63363	4821		
HA-1	145							1168	0	153618	13667	0	42807	1588	36000	6237		
LUCC-7	145							1456	123	36725	13171	11116	27584	1929	27441	4551		
SW-400-28	145							4478	0	350827	13751	7224	23647	2174	26851	5824		
SW-400-28	144							6387	0	247414	15145	16137	24533	4186	36230	5242		
SW-400-28	143							6501	0	436865	14665	4434	30762	7048	23001	5242		
SW-400-28	142							5633	377	43470	12306	40599	4573	2784	30962	7132		
SW-400-28	141							2945	331	331865	18906	13917	13814	7051	20577	7390		
SW-400-28	140							5187	0	452555	14372	8250	17403	4478	34738	10741		
SW-400-28	139							8098	0	403448	18070	10670	21327	8324	45060	7827		
SW-400-28	138							5349	0	354029	18796	8358	17491	4058	27736	7048		
SW-400-28	137							11820	204	1878664	23713	10733	23814	5108	28010	7615		
SW-400-28	136							1336	1562	20533	21185	7532	9182	4081	42027	8604		
SW-400-28	135							3487	0	184818	13980	7369	8048	4063	33408	5702		
SW-400-28	134							2784	0	286236	17780	8672	12644	3047	34175	8455		
SW-400-28	133							1070	2207	386006	17588	5751	10030	3671	67382	4777		
SW-400-28	132							9882	177	84811	18456	10368	8436	4663	35906	5785		
SW-400-28	131							12090	0	48824	14186	4678	6473	3560	35906	5785		
SW-400-28	130							5633	216	468813	17818	7130	11090	3324	40444	8668		
SW-400-28	129							18578	130	30580	12131	3150	3640	2261	37777	2307		
SW-400-28	128							3046	722	712648	12748	8869	13345	4793	35267	8455		
SW-400-28	127							2451	257	420381	13247	3620	20181	2643	37958	4527		
SW-400-28	126							9123	0	84349	18090	41974	17229	4374	39104	6293		
SW-400-28	125							2278	0	272836	18399	9418	20799	1191	5069	5696		
SW-400-28	124							11442	3	137022	6884	63201	24737	5796	32578	4788		
SW-400-28	123							8263	0	440040	12789	10211	15496	2988	26308	4478		
SW-400-28	122							4384	0	440040	12789	10211	15496	2988	26308	4478		
SW-400-28	121							3620	568	1005325	18534	8752	41980	3163	49037	8026		
SW-400-28	120							2186	786	804133	14187	8845	14023	5340	54135	9030		
SW-400-28	119							2854	3587	4964335	16528	8049	112387	8041	125081	2007		
SW-400-28	118							4810	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	117							53714	0	5131454	10374	7084	11828	1111	25178	3702		
SW-400-28	116							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	115							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	114							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	113							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	112							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	111							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	110							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	109							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	108							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	107							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	106							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	105							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	104							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	103							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	102							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	101							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	100							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	99							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	98							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	97							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	96							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	95							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	94							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	93							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	92							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	91							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	90							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	89							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	88							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	87							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	86							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	85							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	84							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	83							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	82							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	81							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	80							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	79							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	78							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	77							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	76							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	75							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	74							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	73							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	72							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	71							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	70							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	69							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	68							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	67							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	66							4819	0	3569707	21767	9518	81843	5968	36180	4314		
SW-400-28	65							4819	0	356970								

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	Turnout - ym	Turnout - fm	Turnout - sp	Turnout - galls	Normal	Enduc	537	SEC 003	AMEO 3	TRM SEC 006	AMEO 8	AMEO 9	CASE SEC 11	EP SEC 12	PK SEC 14	HMSO 16	RS
DeFeng-7								4691	4152	130751	68077	0	0	0	0	0	0
DeFeng-8								1942	351	122184	31568	0	0	0	0	0	0
DeFeng-9								1704	352	23137	22363	0	0	0	0	0	0
DeFeng-11								2064	2910	26836	24352	0	0	0	0	0	0
DeFeng-12								1471	0	143418	14784	0	0	0	0	0	0
DeFeng-10								1137	11437	58719	25013	0	0	0	0	0	0
DeFeng-1								1608	0	176675	87321	0	0	0	0	0	0
DeFeng-2								778	282	80117	44171	0	0	0	0	0	0
DeFeng-3								1028	5099	58418	23252	0	0	0	0	0	0
DeFeng-4								44	3575	46050	15430	0	0	0	0	0	0
DeFeng-5								447	217	37704	9958	0	0	0	0	0	0
DeFeng-6								1754	0	104257	24586	0	0	0	0	0	0
AS18-6								wt	141	1553	20514	11780	0	0	0	0	0
EXVX-8								mutant	201	8465	74732	34175	0	0	0	0	0
HCT-118-7								wt	458	0	48374	15406	0	0	0	0	0
HCT-118-8								wt	365	848	95840	25676	0	0	0	0	0
HT29-1								mutant	293	3501	23134	10610	0	0	0	0	0
HT29-7								mutant	78	3147	6967	6461	0	0	0	0	0
HT29-17								mutant	181	467	80792	18019	0	0	0	0	0
SF539-7								wt	7388	378	15224	64177	0	0	0	0	0
SF539-8								wt	0	0	57678	8734	0	0	0	0	0
SF-268-7								mutant	507	448	33057	13115	0	0	0	0	0
SF-268-8								mutant	802	0	30102	8441	0	0	0	0	0
OVCA4-7								wt	48	107	12107	14682	0	0	0	0	0
OVCA4-4-7								mutant	1389	527	105548	21701	0	0	0	0	0
OVCA4-4-5								mutant	0	329	32948	10780	0	0	0	0	0
OVCA4-5-7								mutant	156	0	17818	10967	0	0	0	0	0
OVCA4-5-8								wt	445	740	24180	11852	0	0	0	0	0
MCJ-7-8								mutant	822	3013	12554	17722	0	0	0	0	0
ADRNES-8								HPV E6	0	2243	23862	8106	0	0	0	0	0
SW460-7								mutant	727	1081	24521	12311	0	0	0	0	0
SW460-8								mutant	226	1200	43102	86009	0	0	0	0	0
H1298-8								mutant	102	2363	53893	10761	0	0	0	0	0
C3A-7								mutant	372	3125	11403	8	0	0	0	0	0
C3A-8								mutant	2	38317	18870	0	0	0	0	0	0
UZOS-7								mutant	20	2184	72622	14777	0	0	0	0	0
UZOS-8								mutant	87	0	154867	8029	0	0	0	0	0
UZOS-9								wt	539	4028	29229	10466	0	0	0	0	0
Hu68-7								wt	8017	4487	24737	14258	0	0	0	0	0
Hu68-8								wt	232	87	9236	7518	0	0	0	0	0
WI38-8								wt	8548	0	615446	26823	15278	11620	3325	37888	7050
AS4 normal RNA								wt	110	0	2070	1153	487	2881	1237	25594	2080
CRL1572 3/17/89								wt	346	1376	88918	7421	4939	12083	23303	59610	5220
Bea-1								mutant	173	504	87915	9767	4804	8347	916	32554	7866
HT298								wt	457	545	18808	8354	4054	4910	728	37354	5760
HT29-1								wt	3176	0	88740	34038	7565	18311	2526	76812	7937
HT29-3								wt	0	300	86186	6334	704	7808	2308	21762	8907
HT29-4								wt	40	608	9337	3342	193	2025	795	33871	4263
Bea-3								wt	8	420	8094	1233	1065	863	751	10850	1689
Bea-5								wt	325	0	8201	5220	519	1788	715	30076	4336
Bea-9								wt	1003	0	10466	12818	1836	1118	1942	30327	4263
Bea-10								wt	881	0	84881	5206	1512	8229	2251	43182	5763
Bea-11								wt	138	0	188113	9608	183	15018	1115	36828	14731
HT29-1								wt	615	0	27263	8036	1535	3034	4090	44374	8188
h Revtrans 3/3/82 P13								wt	384	37	7733	5219	1546	267	400	23075	54
mutant								wt	408	0	286979	11862	2186	10484	1629	24878	4588
MAKRO-QS poly A+								wt	1201	0	31774	11088	2632	1808	1545	27097	4726
SA-OS (Rumy) poly A+								wt	1880	354	75322	17989	3824	3418	2424	32134	7179
MC poly A+								wt	420	2054	84564	8849	0	0	0	0	0
HCT-118-3								wt	583	0	56778	9763	0	0	0	0	0
HCT-118-4								wt	259	377	34553	13093	0	0	0	0	0
HCT-118-5								wt	0	249	82380	12786	0	0	0	0	0
HCT-118-6								wt	0	4346	5330	7226	0	0	0	0	0
AS18-6								mutant	302	3771	40988	8411	0	0	0	0	0
HT29-3								mutant	239	0	82563	8837	0	0	0	0	0
EXVX-8								mutant	27	0	88030	8240	0	0	0	0	0
HT29-4								mutant	448	1288	25013	18178	0	0	0	0	0
HT29-8								mutant	309	0	54935	10000	0	0	0	0	0
HT29-9								wt	581	1208	60523	11477	0	0	0	0	0
OVCA4-4-3								wt	329	467	62478	8801	0	0	0	0	0
OVCA4-4-4								wt	362	362	84029	8192	0	0	0	0	0
OVCA4-4-5								wt	0	522	25881	8741	0	0	0	0	0
OVCA4-4-8								wt	391	0	53062	12881	0	0	0	0	0
SF539-2								wt	408	0	34274	15817	0	0	0	0	0
SF539-4								wt	268	1459	18397	12742	0	0	0	0	0
SF539-5								wt	0	817	27897	14894	0	0	0	0	0
SF539-6								mutant	648	2513	53162	8272	0	0	0	0	0
OVCA4-5-3								mutant	0	3046	45469	8046	0	0	0	0	0
OVCA4-5-4								mutant	512	444	8783	7282	0	0	0	0	0
OVCA4-5-6								mutant	215	992	18534	7377	0	0	0	0	0
ADRNES-8								wt	711	2112	86711	12218	0	0	0	0	0
MCJ-7-8								wt	0	0	52480	16788	0	0	0	0	0
Hu68-6								mutant	312	354	21098	11587	0	0	0	0	0
H1298-8								mutant	829	226	50558	9787	0	0	0	0	0
SW460-3								wt	84	3044	17848	1705	0	0	0	0	0
SW460-4								mutant	0	0	54510	25326	0	0	0	0	0
SW460-5								mutant	0	240	58019	23858	0	0	0	0	0
SW460-6								mutant	858	0	88096	21184	0	0	0	0	0
C3A-3								mutant	258	0	12219	25114	0	0	0	0	0
C3A-4								mutant	426	211	77746	11323	0	0	0	0	0
C3A-5								mutant	144	675	18318	8454	0	0	0	0	0
C3A-6								wt	353	0	8295	7837	0	0	0	0	0
Hu68-8								wt	0	0	21729	30912	0	0	0	0	0
UZOS-3								mutant	917	2742	145703	12520	0	0	0	0	0
UZOS-4								mutant	833	1378	81555	17426	0	0	0	0	0
UZOS-5								wt	454	639	110718	12755	0	0	0	0	0
UZOS-6								mutant	26	4047	6099	8025	0	0	0	0	0
WI38-8								wt	232	4744	87180	10944	0	0	0	0	0
Hu68-3								wt	1338	1334	57079	17844	0	0	0	0	0
Hu68-4								wt	1781	740	80505	27837	0	0	0	0	0
SF-268-3								mutant	1145	8462	18957	21808	0	0	0	0	0
SF-268-4								mutant	821	1850	40530	20121	0	0	0	0	0
SF-268-5								mutant	574	890	55521	12472	0	0	0	0	0
SF-268-6								mutant	1771	1828	127330	48048	0	0	0	0	0
DeFeng-13								wt	1817								

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Table 3 (cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - lb	Tumor - cels	Normal	Endoc	p53	SEQ 17	ANEO 20	SEQ 22	PTN60 24	ANEO 29	DRSEQ 31	DRSEQ 32	ANEO 40	MASEQ 44	T
GMB-1				166				256411			727	871	41121				0
TPB-1				168				43253	715	1044	2483	2283	8374	109			89
T-47D				169				52723	0	4622	838	771	1518	1109			124
Kem-3				171				30043	47	218	800	0	88	0			0
CRL 1641 RNA B30				181				11959	0	486	1871	242	339	32			176
T811 Unselected - D19m				183				21316	0	0	0	0	0	0			120
KB poly A+				184				23563	184	0	1630	2000	1064	365			0
HOS poly A+				186				38104	0	0	1156	3112	1882	145			30
ACH8				188				23810	0	1824	1080	523	874	1750			120
UACC-57				200				14725	130	99	1284	812	845	0			559
MACF-7/ADR-RES				202				12881	314	0	714	495	215	178			426
UTOS (Auntz) poly A+				204				8405	0	0	1294	572	148	0			887
W1591 (Colony) poly A+				206				15922	0	0	14	0	82	0			208
438 endo. cell RNA				208				83548	0	1041	3500	14092	411	0			411
CO137 RNA 3/1/84				218				21193	0	683	0	831	47	0			496
W1-36 72h 0.5%FBS, 24h 10% FBS				219				26009	0	0	0	2727	0	149			124
CRL 1441 - TPA (2h) B30				220				14725	0	123	0	0	355	862			0
Kem-1				221				28116	84	8	1488	336	447	157			381
Kem-2				223				32946	30	0	253	0	233	0			0
KOP-82				225				37338	43	804	154	0	22	0			887
MACF-7				241				22249	0	0	59	726	740	63			0
MACF-7				242				18708	0	12383	1421	22	3944	636			50
BRVX				243				22457	367	303	1636	537	2757	371			0
PA-80				244				33145	0	0	0	0	4253	2803			0
NOG-42				245				28042	860	801	308	307	852	1115			1434
RPMA 8226				246				34425	0	0	2091	567	1814	134			60
ASB-WATCC				247				34516	0	0	683	0	153	0			461
SR				248				18506	0	1351	0	354	730	0			897
OVCA-3				249				27443	30	200	689	853	1417	284			2625
HCT-15				250				34819	0	5278	813	1806	2385	1074			308
OVCA-4				251				10337	478	1077	153	587	81	718			0
UO-31				252				13456	0	415	0	262	757	0			118
OVCA-3				253				80297	0	3782	1757	584	7068	535			1034
SH-3C				254				24530	1119	0	204	483	0	0			0
OVCA-8				255				18487	158	372	582	512	213	819			184
LUX BMV				256				45485	0	18604	0	784	6133	0			278
IGROV-1				257				36126	121	200	740	373	1340	390			231
SK-MEL-2				258				34375	233	280	16716	0	136	377			73
SK-OV-3				259				17172	282	0	0	312	584	0			157
SK-MEL-5				260				138271	212	508	0	1411	339	0			34
SP-539				261				34521	856	1771	624	3454	0	0			650
SK-MEL-28				262				34495	0	3271	817	1130	2425	0			282
BC-462				263				30125	198	11139	0	178	2899	588			336
UACC-257				264				25143	164	0	805	210	817	97			812
M15				265				10120	48	34	0	0	278	0			0
MACF-7				267				68833	0	2892	489	607	1109	2556			448
MDA-MB-435				269				28815	0	878	815	40	503	5			0
HT279				270				34340	0	0	556	7537	0	0			1472
MDA-MB-231				271				37574	727	7043	0	0	492	2143			424
V79 poly A+				273				102305	872	2309	0	802	886	534			1396
HTB36 poly A+				289				28903	44	0	8054	8293	4347	3063			1477
HTB36 24h TPA RNA B2/3				290				47427	0	0	550	2518	0	0			3111
HELA-EAP-631899				313				18309	0	0	0	0	31	299			42
HTB36 On RNA				322				62968	909	0	7168	17280	2781	1124			603
HT347				323				40970	186	787	2353	18699	0	1452			137
438 endo. cell RNA				324				50208	0	177	0	182	5011	0			840
NCI-H220				326				22074	0	184	757	0	334	408			128
HOP-82				327				15894	0	182	1038	1027	2385	1532			231
MDA-MB-231				328				35092	0	8047	14542	11507	1883	5581			1838
U251				330				32858	0	10509	13847	7782	63006	10227			1071
PT cells poly A+				340				11867	71	168	0	0	1433	0			40
MDA-MB-231				341				28466	136	283	2489	823	813	386			202
HCC-2995				343				17789	0	8611	1231	333	873	20			423
SW-620				345				15302	0	818	1383	588	203	461			1336
HT152				346				42840	97	0	2671	17386	2232	1485			849
COLO 205				347				12549	0	0	2185	119	0	0			737
HT219				348				28225	0	0	363	8440	0	0			0
KM-12				349				21716	0	1595	2179	778	350	0			531
HT151				350				40968	860	8470	2432	8252	43	406			211
A498				351				29823	0	182	4815	0	152	803			808
HT303				352				83325	483	0	8725	15803	2090	0			0
RJF 383				353				25449	0	0	1811	337	2050	212			425
TK-10				354				42815	224	6535	2202	8242	8620	2400			231
MDA-MB-3A				357				74434	551	81043	18863	11088	31229	8542			1250
Hs 5787				358				23715	71	2207	1808	824	1418	425			372
HT213				360				41278	0	0	508	262	12710	298			0
HT289				362				34534	510	0	3496	38448	256	0			0
HT139				364				37401	506	213	1871	0	0	1041			55
HT155				366				37790	0	0	784	12374	28	0			281
HT163				367				38672	0	0	734	4844	0	0			489
HT170				368				58844	781	0	7384	55230	87	8077			620
HT172				369				21375	87	0	871	3817	0	0			638
HT138				370				41851	0	243	17086	0	1711	0			0
HT118				371				37707	0	0	298	1891	78	0			443
HT154				372				32270	0	0	11729	0	885	0			183
HT180				373				20571	81	0	801	3611	663	73			2343
HT180				374				20113	0	0	2863	1192	2444	0			1826
HT180				375				27825	267	0	1224	35	358	725			704
HT143				376				20412	0	475	285	0	0	0			297
HT186				377				18360	135	0	432	8121	0	0			558
HT145				378				27515	873	0	7847	22822	0	0			231
HT227				379				30806	0	0	2485	278	423	0			5373
HT302				380				37705	0	0	1867	71833	761	0			2001
HT314				381				38827	475	0	131	18658	313	0			0
HT317				382				65236	818	0	8015	62588	2053	0			420
MDA-MB-231 8128 11/8				383				30484	0	0	142	119	0	266			0
HT323				384				51644	187	638	0	13817	0	0			0
HT337				385				43118	156	0	786	7545	87	163			849
HT335				386				47983	0	178	0	3120	9	330			180
HT148				387				13508	209	0	0	2507	0	183			36
HT348				388				51448	631	0	182	14207	0	128			728
HT311																	



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Table 3 (cont'd)

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Table 3 (cont'd)

Time	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100																																																		
150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300

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Table 3 (cont'd)

Tissue	Tumor-eyn	Normal-eyn	Tumor-ta	Tumor-cell	Normal	Enos	p22	SEQ 17	AASEQ 29	SCSEQ 23	PTRSQ 24	AASEQ 30	DISEQ 31	DISEQ 32	AASEQ 33	MASEQ 34
Dafang-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-75	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-78	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-79	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-80	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-81	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-82	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-83	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-85	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-86	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-88	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-90	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-91	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-92	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-93	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-94	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-95	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-96	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-97	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-99	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dafang-100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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Table 3 (cont'd)

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174  
Table 3 (cont'd)[illegible]

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175  
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176  
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177  
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Table 3 (cont'd)

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179  
Table 3 (cont'd)

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180  
Table 3 (cont'd)[illegible]

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Table 3 (cont'd)

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Tissue	Tumor type	Number of tumors	Tumor size	Tumor cells	Normal	Endoth	p53	SE0	SE1	SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9	SE10	SE11	SE12	SE13	SE14	SE15	SE16	SE17	SE18	SE19	SE20	SE21	SE22	SE23	SE24	SE25	SE26	SE27	SE28	SE29	SE30	SE31	SE32	SE33	SE34	SE35	SE36	SE37	SE38	SE39	SE40	SE41	SE42	SE43	SE44	SE45	SE46	SE47	SE48	SE49	SE50	SE51	SE52	SE53	SE54	SE55	SE56	SE57	SE58	SE59	SE60	SE61	SE62	SE63	SE64	SE65	SE66	SE67	SE68	SE69	SE70	SE71	SE72	SE73	SE74	SE75	SE76	SE77	SE78	SE79	SE80	SE81	SE82	SE83	SE84	SE85	SE86	SE87	SE88	SE89	SE90	SE91	SE92	SE93	SE94	SE95	SE96	SE97	SE98	SE99	SE100	SE101	SE102	SE103	SE104	SE105	SE106	SE107	SE108	SE109	SE110	SE111	SE112	SE113	SE114	SE115	SE116	SE117	SE118	SE119	SE120	SE121	SE122	SE123	SE124	SE125	SE126	SE127	SE128	SE129	SE130	SE131	SE132	SE133	SE134	SE135	SE136	SE137	SE138	SE139	SE140	SE141	SE142	SE143	SE144	SE145	SE146	SE147	SE148	SE149	SE150	SE151	SE152	SE153	SE154	SE155	SE156	SE157	SE158	SE159	SE160	SE161	SE162	SE163	SE164	SE165	SE166	SE167	SE168	SE169	SE170	SE171	SE172	SE173	SE174	SE175	SE176	SE177	SE178	SE179	SE180	SE181	SE182	SE183	SE184	SE185	SE186	SE187	SE188	SE189	SE190	SE191	SE192	SE193	SE194	SE195	SE196	SE197	SE198	SE199	SE200	SE201	SE202	SE203	SE204	SE205	SE206	SE207	SE208	SE209	SE210	SE211	SE212	SE213	SE214	SE215	SE216	SE217	SE218	SE219	SE220	SE221	SE222	SE223	SE224	SE225	SE226	SE227	SE228	SE229	SE230	SE231	SE232	SE233	SE234	SE235	SE236	SE237	SE238	SE239	SE240	SE241	SE242	SE243	SE244	SE245	SE246	SE247	SE248	SE249	SE250	SE251	SE252	SE253	SE254	SE255	SE256	SE257	SE258	SE259	SE260	SE261	SE262	SE263	SE264	SE265	SE266	SE267	SE268	SE269	SE270	SE271	SE272	SE273	SE274	SE275	SE276	SE277	SE278	SE279	SE280	SE281	SE282	SE283	SE284	SE285	SE286	SE287	SE288	SE289	SE290	SE291	SE292	SE293	SE294	SE295	SE296	SE297	SE298	SE299	SE300	SE301	SE302	SE303	SE304	SE305	SE306	SE307	SE308	SE309	SE310	SE311	SE312	SE313	SE314	SE315	SE316	SE317	SE318	SE319	SE320	SE321	SE322	SE323	SE324	SE325	SE326	SE327	SE328	SE329	SE330	SE331	SE332	SE333	SE334	SE335	SE336	SE337	SE338	SE339	SE340	SE341	SE342	SE343	SE344	SE345	SE346	SE347	SE348	SE349	SE350	SE351	SE352	SE353	SE354	SE355	SE356	SE357	SE358	SE359	SE360	SE361	SE362	SE363	SE364	SE365	SE366	SE367	SE368	SE369	SE370	SE371	SE372	SE373	SE374	SE375	SE376	SE377	SE378	SE379	SE380	SE381	SE382	SE383	SE384	SE385	SE386	SE387	SE388	SE389	SE390	SE391	SE392	SE393	SE394	SE395	SE396	SE397	SE398	SE399	SE400	SE401	SE402	SE403	SE404	SE405	SE406	SE407	SE408	SE409	SE410	SE411	SE412	SE413	SE414	SE415	SE416	SE417	SE418	SE419	SE420	SE421	SE422	SE423	SE424	SE425	SE426	SE427	SE428	SE429	SE430	SE431	SE432	SE433	SE434	SE435	SE436	SE437	SE438	SE439	SE440	SE441	SE442	SE443	SE444	SE445	SE446	SE447	SE448	SE449	SE450	SE451	SE452	SE453	SE454	SE455	SE456	SE457	SE458	SE459	SE460	SE461	SE462	SE463	SE464	SE465	SE466	SE467	SE468	SE469	SE470	SE471	SE472	SE473	SE474	SE475	SE476	SE477	SE478	SE479	SE480	SE481	SE482	SE483	SE484	SE485	SE486	SE487	SE488	SE489	SE490	SE491	SE492	SE493	SE494	SE495	SE496	SE497	SE498	SE499	SE500	SE501	SE502	SE503	SE504	SE505	SE506	SE507	SE508	SE509	SE510	SE511	SE512	SE513	SE514	SE515	SE516	SE517	SE518	SE519	SE520	SE521	SE522	SE523	SE524	SE525	SE526	SE527	SE528	SE529	SE530	SE531	SE532	SE533	SE534	SE535	SE536	SE537	SE538	SE539	SE540	SE541	SE542	SE543	SE544	SE545	SE546	SE547	SE548	SE549	SE550	SE551	SE552	SE553	SE554	SE555	SE556	SE557	SE558	SE559	SE560	SE561	SE562	SE563	SE564	SE565	SE566	SE567	SE568	SE569	SE570	SE571	SE572	SE573	SE574	SE575	SE576	SE577	SE578	SE579	SE580	SE581	SE582	SE583	SE584	SE585	SE586	SE587	SE588	SE589	SE590	SE591	SE592	SE593	SE594	SE595	SE596	SE597	SE598	SE599	SE600	SE601	SE602	SE603	SE604	SE605	SE606	SE607	SE608	SE609	SE610	SE611	SE612	SE613	SE614	SE615	SE616	SE617	SE618	SE619	SE620	SE621	SE622	SE623	SE624	SE625	SE626	SE627	SE628	SE629	SE630	SE631	SE632	SE633	SE634	SE635	SE636	SE637	SE638	SE639	SE640	SE641	SE642	SE643	SE644	SE645	SE646	SE647	SE648	SE649	SE650	SE651	SE652	SE653	SE654	SE655	SE656	SE657	SE658	SE659	SE660	SE661	SE662	SE663	SE664	SE665	SE666	SE667	SE668	SE669	SE670	SE671	SE672	SE673	SE674	SE675	SE676	SE677	SE678	SE679	SE680	SE681	SE682	SE683	SE684	SE685	SE686	SE687	SE688	SE689	SE690	SE691	SE692	SE693	SE694	SE695	SE696	SE697	SE698	SE699	SE700	SE701	SE702	SE703	SE704	SE705	SE706	SE707	SE708	SE709	SE710	SE711	SE712	SE713	SE714	SE715	SE716	SE717	SE718	SE719	SE720	SE721	SE722	SE723	SE724	SE725	SE726	SE727	SE728	SE729	SE730	SE731	SE732	SE733	SE734	SE735	SE736	SE737	SE738	SE739	SE740	SE741	SE742	SE743	SE744	SE745	SE746	SE747	SE748	SE749	SE750	SE751	SE752	SE753	SE754	SE755	SE756	SE757	SE758	SE759	SE760	SE761	SE762	SE763	SE764	SE765	SE766	SE767	SE768	SE769	SE770	SE771	SE772	SE773	SE774	SE775	SE776	SE777	SE778	SE779	SE780	SE781	SE782	SE783	SE784	SE785	SE786	SE787	SE788	SE789	SE790	SE791	SE792	SE793	SE794	SE795	SE796	SE797	SE798	SE799	SE800	SE801	SE802	SE803	SE804	SE805	SE806	SE807	SE808	SE809	SE810	SE811	SE812	SE813	SE814	SE815	SE816	SE817	SE818	SE819	SE820	SE821	SE822	SE823	SE824	SE825	SE826	SE827	SE828	SE829	SE830	SE831	SE832	SE833	SE834	SE835	SE836	SE837	SE838	SE839	SE840	SE841	SE842	SE843	SE844	SE845	SE846	SE847	SE848	SE849	SE850	SE851	SE852	SE853	SE854	SE855	SE856	SE857	SE858	SE859	SE860	SE861	SE862	SE863	SE864	SE865	SE866	SE867	SE868	SE869	SE870	SE871	SE872	SE873	SE874	SE875	SE876	SE877	SE878	SE879	SE880	SE881	SE882	SE883	SE884	SE885	SE886	SE887	SE888	SE889	SE890	SE891	SE892	SE893	SE894	SE895	SE896	SE897	SE898	SE899	SE900	SE901	SE902	SE903	SE904	SE905	SE906	SE907	SE908	SE909	SE910	SE911	SE912	SE913	SE914	SE915	SE916	SE917	SE918	SE919	SE920	SE921	SE922	SE923	SE924	SE925	SE926	SE927	SE928	SE929	SE930	SE931	SE932	SE933	SE934	SE935	SE936	SE937	SE938	SE939	SE940	SE941	SE942	SE943	SE944	SE945	SE946	SE947	SE948	SE949	SE950	SE951	SE952	SE953	SE954	SE955	SE956	SE957	SE958	SE959	SE960	SE961	SE962	SE963	SE964	SE965	SE966	SE967	SE968	SE969	SE970	SE971	SE972	SE973	SE974	SE975	SE976	SE977	SE978	SE979	SE980	SE981	SE982	SE983	SE984	SE985	SE986	SE987	SE988	SE989	SE990	SE991	SE992	SE993	SE994	SE995	SE996	SE997	SE998	SE999	SE1000	SE1001	SE1002	SE1003	SE1004	SE1005	SE1006	SE1007	SE1008	SE1009	SE1010	SE1011	SE1012	SE1013	SE1014	SE1015	SE1016	SE1017	SE1018	SE1019	SE1020	SE1021	SE1022	SE1023	SE1024	SE1025	SE1026	SE1027	SE1028	SE1029	SE1030	SE1031	SE1032	SE1033	SE1034	SE1035	SE1036	SE1037	SE1038	SE1039	SE1040	SE1041	SE1042	SE1043	SE1044	SE1045	SE1046	SE1047	SE1048	SE1049	SE1050	SE1051	SE1052	SE1053	SE1054	SE1055	SE1056	SE1057	SE1058	SE1059	SE1060	SE1061	SE1062	SE1063	SE1064	SE1065	SE1066	SE1067	SE1068	SE1069	SE1070	SE1071	SE1072	SE1073	SE1074	SE1075	SE1076	SE1077	SE1078	SE1079	SE1080	SE1081	SE1082	SE1083	SE1084	SE1085	SE1086	SE1087	SE1088	SE1089	SE1090	SE1091	SE1092	SE1093	SE1094	SE1095	SE1096	SE1097	SE1098	SE1099	SE1100	SE1101	SE1102	SE1103	SE1104	SE1105	SE1106	SE1107	SE1108	SE1109	SE1110	SE1111	SE1112	SE1113	SE1114	SE1115	SE1116	SE1117	SE1118	SE1119	SE1120	SE1121	SE1122	SE1123	SE1124	SE1125	SE1126	SE1127	SE1128	SE1129	SE1130	SE1131	SE1132	SE1133	SE1134	SE1135	SE1136	SE1137	SE1138	SE1139	SE1140	SE1141	SE1142	SE1143	SE1144	SE1145	SE1146	SE1147	SE1148	SE1149	SE1150	SE1151	SE1152	SE1153	SE1154	SE1155	SE1156	SE1157	SE1158	SE1159	SE1160	SE1161	SE1162	SE1163	SE1164	SE1165	SE1166	SE1167	SE1168	SE1169	SE1170	SE1171	SE1172	SE1173	SE1174	SE1175	SE1176	SE1177	SE1178	SE1179	SE1180	SE1181	SE1182	SE1183	SE1184	SE1185	SE1186	SE1187	SE1188	SE1189	SE1190	SE1191	SE1192	SE1193	SE1194	SE1195	SE1196	SE1197	SE1198	SE1199	SE1200	SE1201	SE1202	SE1203	SE1204	SE1205	SE1206	SE1207	SE1208	SE1209	SE1210	SE1211	SE1212	SE1213	SE1214	SE1215	SE1216	SE1217	SE1218	SE1219	SE1220	SE1221	SE1222	SE1223	SE1224	SE1225	SE1226	SE1227	SE1228	SE1229	SE1230	SE1231	SE1232	SE1233	SE1234	SE1235	SE1236	SE1237	SE1238	SE1239	SE1240	SE1241	SE1242	SE1243	SE1244	SE1245	SE1246	SE1247	SE1248	SE1249	SE1250	SE1251	SE1252	SE1253	SE1254	SE1255	SE1256	SE1257	SE1258	SE1259	SE1260	SE1261	SE1262	SE1263	SE1264	SE1265	SE1266	SE1267	SE1268	SE1269	SE1270	SE1271	SE1272	SE1273	SE1274	SE1275	SE1276	SE1277	SE1278	SE1279	SE1280	SE1281	SE1282	SE1283	SE1284	SE1285	SE1286	SE1287	SE1288	SE1289	SE1290	SE1291	SE1292	SE1293	SE1294	SE1295	SE1296	SE1297	SE1298	SE1299	SE1300	SE1301	SE1302	SE1303	SE1304	SE1305	SE1306	SE1307	SE1308	SE1309	SE1310	SE1311	SE1312	SE1313	SE1314	SE1315	SE1316	SE1317	SE1318	SE1319	SE1320	SE13
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Table 3 (cont'd)

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Table 3<sup>188</sup> (cont'd)

Tissue	Tumor type	Normal type	Tumor - 1a	Tumor cells	Normal	Endoth	p23	SEQ 118 3
DAL-1				185				4
T-470				185				0
U-3				171				0
CRL 1441 RNA 8/00				181				72
761T untreated + DNase				183				0
CB poly A+				178				189
HCS poly A+				195				47
ACHN				198				0
UACC-82				200				53
ANCF-1/ADR-RES				202				0
UTOS (Mundy) poly a+				204				0
WISH (Collagen) poly A+				205				38
458 muscle mRNA				205				34
COL137 RNA 3/2/89				205				200
W130 T2h 0.5% FBS, 3h 10% FBS				213				0
CRL 1441 + TPA (2h) 8/00				213				0
Ren-1				220				242
Ren-2				221				46
Ren-3				222				0
MDA-MB-435				222				0
SK-VI				242				0
SK-MEL-3				243				0
NCI-H20				244				0
RPMI 8226				245				0
458WATCC				246				0
SK				247				241
OVCA9-3				248				0
HCT-116				249				0
OVCA9-4				250				85
UO-31				251				0
OVCA9-5				252				0
SHYX				253				0
OVCA9-6				254				248
LO2 BM1				255				0
IGROV1				256				0
SK-MEL-3				257				0
SK-OV-3				258				0
SK-MEL-3				259				153
SK-SB				260				0
SK-MEL-28				261				0
H-562				262				0
UACC-257				263				0
SK-14				264				0
ANCF7				265				23
MDA-MB-435				267				0
HT779				268				49
MDA-MB				269				189
17B poly A+				270				0
ANCF poly A+				271				0
HT1336 2h TPA RNA 9/00				272				0
MDA-MB-435				273				0
MDA-MB-435				274				26
HT1336 2h RNA				275				147
HT1336				276				83
458 muscle RNA				277				0
NCI-H20				278				0
MDA-MB-231				279				155
UO-31				280				0
HT1336 poly A+				281				0
MDA-MB-435				282				81
MDA-MB-435				283				0
MDA-MB-435				284				0
MDA-MB-435				285				0
MDA-MB-435				286				0
MDA-MB-435				287				0
MDA-MB-435				288				0
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MDA-MB-435				293				0
MDA-MB-435				294				0
MDA-MB-435				295				0
MDA-MB-435				296				0
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MDA-MB-435				300				0
MDA-MB-435				301				0
MDA-MB-435				302				0
MDA-MB-435				303				0
MDA-MB-435				304				0
MDA-MB-435				305				0
MDA-MB-435				306				0
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MDA-MB-435				372				0
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MDA-MB-435				376				0
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MDA-MB-435				385				0
MDA-MB-435				386				0
MDA-MB-435				387				0
MDA-MB-435				388				0
MDA-MB-435				389				0
MDA-MB-435				390				0
MDA-MB-435				391				0
MDA-MB-435				392				0
MDA-MB-435				393				0
MDA-MB-435				394				0
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MDA-MB-435				400				0
MDA-MB-435				401				0
MDA-MB-435				402				0
MDA-MB-435				403				0
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MDA-MB-435				405				0
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MDA-MB-435				424				0
MDA-MB-435				425				0
MDA-MB-435				426				0
MDA-MB-435				427				0
MDA-MB-435				428				0
MDA-MB-435				429				0
MDA-MB-435				430				0
MDA-MB-435				431				0
MDA-MB-435				432				0
MDA-MB-435				433				0
MDA-MB-435				434				0
MDA-MB-435				435				0
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MDA-MB-435				438				0
MDA-MB-435				439				0
MDA-MB-435				440				0
MDA-MB-435				441				0
MDA-MB-435				442				0
MDA-MB-435				443				0
MDA-MB-435								

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Table 3 (cont'd)

Time	Turner - sym	Normal - sym	Turner - la	Turner - cells	Normal	Endus	p52	SEG 1% S
MIL-211	155							0
MIL-21A-DLRES	182							7
MCF-7	191							22
MIL-7	149							5
MIL-7	147							53
LACC-267	145							53
LACC-82	144							91
SK-MEL-28	143							263
UG-31	142							378
SH-MEL-3	141							181
KM-12	140							250
SK-MEL-2	139							181
HCT-15	138							250
Human JM	137							0
COLO 205	136							0
COLI MAY	135							0
SW-620	134							82
Tx-10	133							278
HCT 116	132							0
TIB-4	131							300
HCC-959	130							89
AACHN	129							278
PC-1	128							0
RUF-380	127							0
DLL145	126							317
Cabo-1	125							0
3B	124							120
AMR8	123							118
HPM 82X	122							0
S.H.KC	121							0
H-40	120							36
MCL-4	119							142
OVCAR-5	118							898
K-M2	117							181
OVCAR-4	116							87
COSMIC	115							0
OVCAR-3	114							181
SF-639	113							180
HGP-A2	112							132
SF-209	111							0
ASHBATCC	110							204
SF-261	109							0
HCAH-2	108							30
UC31	107							400
HCL-H802	106							78
GAB-15	105							62
HCL-H22M	104							0
SMB-19	103							54
NCAH-208	102							0
SK-OV-3	101							0
NCLH2	100							43
BROPI	99							148
BOVA	98							238
OVCAR-4	97							130
MCF-82	96							0
n.h.m.s.c.a.m. 102/104 #17	95							0
n.h.m.s.c.a.m. 102/104 #10	94							0
n.h.m.s.c.a.m. 102/104 #10	93							0
TCSP	92							379
AS48-1	91							458
AS48-3	90							347
AS48-4	89							70
AS48-5	88							0
AS48-7	87							290
EOV-1	86							0
EOV-4	85							485
EOV-5	84							877
EOV-7	83							0
MCF-7-1	82							315
MCF-7-2	81							0
MCF-7-3	80							0
MCF-7-4	79							3049
MCF-7-5	78							138
MCF-7-7	77							78
ADR-RES-1	76							18

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Table 3 (cont'd)

Tissue	Turner-sym	Normal-sym	Turner + 1a	Turner calls	Normal	Endoc	p33	SEQ 118.3
DaPang-2								1582
DaPang-4								2991
DaPang-8								850
DaPang-11								2503
DaPang-12								518
DaPang-10								368
DaPang-1								416
DaPang-2								0
DaPang-3								222
DaPang-4								0
DaPang-5								0
DaPang-6								0
AS41-1-8								0
EXV4-8						wt		0
HCT-118-7						mutant		56
HCT-118-8						wt		0
HT29-1						wt		0
HT29-7						mutant		310
HT29-8						mutant		69
SF330-7						mutant		153
SF330-8						wt		0
SF-398.7						mutant		0
SF-398.4						wt		209
OVCA4-7						mutant		218
OVCA4-8						mutant		503
OVCA4-6-7						wt		405
OVCA4-8						wt		8
MCF-7-8						mutant		851
ADR-R25-8						mutant		501
Mela-1-8						wt		35
SW480-7						mutant		657
SW480-8						wt		0
H1291-8						mutant		0
C33A-7						mutant		0
C33A-8						mutant		0
U2OS-7						wt		0
U2OS-8						mutant		0
Hs68-7						mutant		729
Hs68-8						mutant		37
Wt 31-8						wt		0
458 medulla RNA						wt		0
GLE 1572 31789						wt		0
Bem-1						wt		0
HT360						wt		71
HT378						wt		221
HT385						wt		80
HT396						wt		191
Bem-2						wt		80
Bem-3						wt		0
Bem-4						wt		0
is he atrocytes 3/25/82 #10						wt		487
Bem-10						wt		175
HT1810						wt		177
A fibroblasts 3/31/82 #12						wt		481
promote, h						wt		237
MBNDCOS poly A+						wt		0
SA-C8 (blumdy) poly A+						wt		0
Mx. poly A+						wt		32
HCT-118-3						wt		0
HCT-118-4						wt		0
HCT-118-5						wt		384
HCT-118-6						wt		0
AS41-4						wt		0
HT29-3						wt		0
EXV4-6						wt		0
HT29-4						mutant		814
HT29-5						mutant		121
HT29-6						mutant		846
OVCA4-3						mutant		0
OVCA4-4						mutant		177
OVCA4-5						wt		339
OVCA4-6						wt		0
SF330-3						wt		18
SF330-4						wt		0
SF330-5						wt		728
SF330-6						wt		82

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Table 4

Extra-Catalytic Domains (Amino acid positions)									
Gene Name	SP ID#	na ID#	aa	Family	Group	Length_AA	Regulator of G protein signalling domain 54-175; PH domain 559-652		
X69117_h_beta_adrene	H	1	122	AGC	GRK	688	Regulator of G protein signalling domain 54-175; PH domain 559-652		
AA144574_m	M	2	123	AGC	GRK	378	PH domain 249-337		
AA210825_h	H	9	130	AGC	PKC	978	Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577		
AA316804_h	H	11	132	AGC	PKC	890	Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532		
AA887783_h	H	21	142	AGC	SGK	446	PX domain 13-120		
AA021445_h_3	H	32	152	CAMK	EMK	1311	Vitamin K-dependent carboxylation/gamma-carboxyglutamic (GLA) domain 1072-1113		
R31237_1_h_AAC3348	H	34	154	CAMK	EMK	729	UBA domain 327-365		
406786.5_h	H	36	156	CAMK	EMK	1330	PAS domain 133-186, 247-280, 354-386		
Z36720_h	H	41	161	CAMK	MLCK	874	WD domain, G-beta repeat 674-711		
SGK086_h	H	42	162	CAMK	Tric	2287	Immunoglobulin domain 1-62, 97-153, 221-277, 518-578, 1617-1678; Fibronectin type III domain 301-390, 1697-1779		
R19772_h	H	44	164	CAMK	Tric	1287	RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 786-851; PH domain 419-528		
17000139801197_h_IRAH	H	76	195	Other	IRAK	596	Death domain 26-106		
AA088547_h	H	78	197	Other	IRE	922	PQQ enzyme repeat 39-76		
AA232253_h	H	82	201	Other	MLK	800	SAM domain (Sterile alpha motif) 337-408		
AA599286_h	H	89	208	Other	SLOB	649	PX domain 16-122		
AA836348_h	H	113	232	STE	NEK	836	Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 598-650		
PAK6_h	H	115	234	STE	STE20-02	719	P21-Rho-binding domain 11-69		

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## FIGURE 1A

SEQ ID NO: 122\_X69117\_H BARK2\_H  
 MADLEAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN  
 QKIGFLLFKDFCLNEINEAVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSC  
 SHPFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDIQKFMESDKFTRFCQWKNV  
 ELNIHMTMNEFSVHRIIGRGGEVYGCRAKDTGKMYAMKCLDKKRIKMQGETLALNER  
 IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYATE  
 IILGLEHVHNRFFVYRDLKPANILLDEHGHAIRISDLGLACDFSKKKPHASVGTGHYMAPE  
 VLQKGTAYDSSADWFSLGCMLFKLLRGHSPFRQHKTDKKHEIDRMTLTVNVELPDTFSPE  
 LKSLLEGLLQORDVSKRLGCHGGGSQEVKEHSFFKGVDWQHVVYLQKYPPLIPPRGEVNAA  
 DAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERWQQEVTETVYEAVNADTDKIEARK  
 RAKNKQLGHEEDYALGKDCIMHGMYMLKGNPFLTQWQRRYFYLFNRLWRGEGESRQNL  
 LTMEQILSVEETQIKDKCILFRIKGGKQFVLQCESDPEFVQWKELNETFKEAQRLLRR  
 APKFLNKPRSGTVELPKPSLCHRNSNGL

SEQ ID NO: 123\_AA144574\_M BARK2\_M  
 CFVVYRDLKPANILLDEYGHVIRISDLGLACDFSKKKPHASVGTGHYMAPEVLQKGTCTYDS  
 SADWFSLGCMLFKLLRGHSPFRQHKTDKKHEIDRMTLTVNVLQPDFAFSPELRSLLEGLLQ  
 RDVSQRLGCGGGGARELKEHIFFKGIDWQHVVYLRYKYPPLIPPRGEVNAAADAFDIGSFDE  
 EDTKGIKLLDCDQDLYKNFPLVISERWQQEVETIYDAVNADTDKIEARKKAKNKQLGQE  
 EDYAMGKDCIMHGMYMLKGNPFLTQWQRRYFYLFNRLWRGEGESRQSLTMEQIMSVE  
 ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLLRRAPKFLNKPR  
 AILEFSKPPPLCHRNSSGL

SEQ ID NO: 124\_AA826850\_H  
 MGSSMSAATARRPVFDDKEDVNFDFHFIQILRAIGKGSFGKVCIVQKRDTEKMYAMKYMKNQ  
 QCIERDEVNRNVFRELEILQEIHEVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQ  
 FSEDTVRLYICEMALALDYLGRQHIHRDVKPDNILLDERGHAHLTDFNIATIIKDGERRA  
 TALAGTKPYMAPEIFXSFGVGGTGYSFEVDWWSVGVMAVELLRGWRPYDIHSSNAVESLV  
 QLFSTVSVQYVPTWSKEMVALLRKLTLVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRV  
 PGFVFNKGRHLCDPTFELEEMILESRLPHKKKKRLAKNRSRDNSSQSENDYLQDCLD  
 AIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCGPICPSAGSG

SEQ ID NO: 125\_AA960957\_H  
 MGGNHSKPPVFDENEEVNFDFHFIQILRAIGKGSFGKVCIVQKRDTKMYAMKYMKNQKCI  
 ERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFT  
 GTVKLYICELALALEYLQRYHIHRDIKPDNILLDEHGHHVITDFNIATVVKGAERASSM  
 AGTKPYMAPEVFQVYMDRGPYSPVDWWSLGITAYELLRGWRPYEIHSTPIDEILNMF  
 KVERVHYSSTWCKGMVALLRKLTKDPESRVSSLHDIQSVPYLADMNWDVFKKALMPGF  
 VFNKGRNLCDPTFELEEMILESRLPHKKKKRLAKNRSRDNSSQSENDYLQDCLD  
 EFIIIFNREKLRRQQGQGSQLLDTSRGGGQAQSKLQDGCNNLLTHTCTRGCS

SEQ ID NO: 126\_TBK1\_H  
 MQSTSNHLWLLSDILGQATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMRFEVFLK  
 KLNHNKIVKLFALIEETTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVV  
 GGMNHLRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVSLEYGTEEYL  
 HPDMYERAVLRKDQKKGATVDLWSIGVTIFYHAATGSLPFRPFEGPRRNKEVMYKIITG  
 KPSSGAISGVQKAENGPIDWSGDMVSCSLSRGLQVLLTPVLANILEADQEKCWGFDQFFA  
 ETSIDLHRMVIHVSFSLQOMTAHKIYIHSYNTATIFHELVIYKQTKIISNQELIYEGRLV  
 LEPGRLAQHFPKTTENPIFVVSREPLNTIGLIYEKISLPKVHPRYDLGDASMAKAITG  
 VVCYACRIASTLLLYQELMRKGIRWLIELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

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## FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWAHQE  
GTHPKDRNVEKLQVLLNCMTEIYYQFKDKAERRLAYNEEQIHKFDKQKLYYHATKAMTH  
FTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNELQETLPQ  
KMFTASSGIKHTMTPIYPSSNTLVEMTLGMKKLKEEMEGVVKELAENNHI LERFGSLTMD  
GGLRNVDCI

SEQ ID NO: 127\_AA305176\_H  
MDPTAGSKKEPGGGAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLQKGGKLYA  
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLOSANNVYLVMEYLIGGDVKS  
LLHIYGYFDEEMAVKYISEVALALDYLRHGI IHRDLKPDNMLI SNEGHI KLTDFGLSKV  
TLNRDINMMDILTTPSMAPRODYSRTPGQVLSLISLGFNTPIAEKNQDPANILSACLS  
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS  
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128\_AA116841\_M  
TRPIPWPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFV  
PQPDDETDTSYFEARNNAQHLTVSGFSL

SEQ ID NO: 129\_AA256100\_H  
MAMTAGTTTTFPMNSNHTRERVTVAKLTLENFYNSNLIQHEERETRQKKLEVAMEEEGLAD  
EEKKLRRSQHARKETEFRLRLKRTLGLDDFESLKVI GRGAFGEVRLVQKDTGHIYAMKI  
LRKSDMLEKEQVAHIRAERDILVEADGAWVVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM  
KKDTLTEEETQFYISETVLAIDAIHQLGFIHRDIKPDNLLLDAGHVKLSDFGLCTGLKK  
AHRTEFYRNLTHNPPSDFSFQNMNSKRKAETWKKNRRLAYSTVGTPTYIAPEVFMQTY  
NKLCDWWSLGVIMYEMLIGYPPFCSETPQETRYKVMNWKETLVFPPEVPISEKADLILR  
FCIDSENRIENSGVEEIKGHPFFEGVDWEHIRERPAIPIEIKSIDDTSNFDDFPESDIL  
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQGRSIPITYMKAGKL

SEQ ID NO: 130\_AA210825\_H  
DSLLPTPALGTPLPI PWPVGSRLTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG  
SPLSHHLLTRSRGSRTOGPPGPPGGSRVGSRRAPVGLPPWPPPPHYAGLPGPSGPGSPP  
PPGGLLEQSPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHVQLACSIVDQKF  
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVVLSASATFEDFQIRPHAL  
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCGLNHYHKRCAFSIPNNCSGARKRRLSSTSL  
ASGHSVRLGTSESPLCTAEELSRSTELLPRRPSSSSSSASSYTGRPIELDKMLLSKV  
KVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDKFNCHKRCATRVPNDCLEALIN  
GDVPMEEATDFSEADKSALMDESEDSGVI PGSHSENALHASEEEEGEGGKAQSSLGYPIL  
MRVVQSVRHTTRKSSTTLREGWVHYSNKDLTKRHYWRLDCKCITLFQNNNTNRYKEI  
PLSEILTVEAQNFSLVPPGTNPHCFEIVTANATYFVGEMPGGTPGGPSGQGAEAARGLX  
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSG  
QFGVVYGGKHKRTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLRHPGIVNLECMFETP  
EKVFVMEKLHGDMLEMILSSEKGRLPRLTKFLITQILVALRHLHFKNIVHCDLKPENV  
LLASADFPQVKLCDFGFARIIGEKSFRRSVGTPAYLAPEVLLNQGYNRSLDMWSVGVI  
MYVSLSGTFPFNEDEDINDQIQNAAFMYPASWHSISAGAIIDLINLLQVKMRKRYSDK  
SLSHPWLOEYQTWLDRLELEGKMGERYITHESDDARWEQFAAEHPLPGSGLPTDRDLGGA  
CPPQDHDMQGLAERISVL

SEQ ID NO: 131\_AA127299\_H  
IQFIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVIKKTLTPTWNETFFVHFPEKTTLEL  
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

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FIGURE 1C

SEQ ID NO: 132\_AA316804\_H  
 MSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSLTNSRGSVHTV  
 SFLLOIGLTRESVTIEAQELSLSAVKDLVCSIVYQKFPÉCGFFGMYDKILLFRHDMNSEN  
 ILQLITSADEIHEGDLVEVVLALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR  
 QGLKCEGCGLNHYHKRCFAFKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLQPEYVALPSEES  
 HVHQEPSKRIPSWSGRPIWMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM  
 QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDNNDINSDSSRGLDDT  
 EEPSPPEDKMFLLDPSDLDERDEEAVKTI SPSTSNIPLMRVVQSIKHTKRKSSTMVKE  
 GWMVHYTSRDNLKRHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQG  
 SNPHCFEIIITDMVYFVGENNGDSSHNPLAATGVGLDVAQSWEKAIRQALMPVTPQASV  
 CTSPGQGDHKLSTSI SVSNCOIQENVDISTVYQIFADEVLGSGQFGIVYGGKHKRKTGR  
 DVAIKVIDKMRFPPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVMEKLHGDMLE  
 EMILSSEKSRLEPERITKFMVTQILVALRNLHFKNIVHCDLKPENVLLASAEPFPQVKLCD  
 FGFARIIGEKSFRRSVGTPAYLAPEVLRSGYNSLDMWSVGVIYVSLSGTFPFNEDE  
 DINDQIQNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSDKSLSHPLWLDYQOTWLD  
 LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133\_PKNBETA\_H  
 MEEGAPRQPGPSQWPPPEDEKEVIRRAIQKELKIKEGVENLRRVATDRRHGLGHVQQLLRSS  
 NRRLEQLHRELRELHARILLPGPGPAEPVASGPRPWAEQLRARHLEALRRQLHVELKV  
 KQGAENMTHTCASGTPKERKLLAAQQLRDSQLKVALLRMKISSLEASGSPEPGPELLA  
 EELQHRLHVEAAVAEGAKNVVLLSSRRTQDRKALAEAAQQLQESSQKLDLLRLALEQLL  
 EQLPPAHPLRSRVTRELRAAVPGYPQPSGTPVKPTALTGTQVRLGCEQLLTAVPGRSP  
 AAALASSPSEGWLRTKAKHQGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI  
 PLERARELEIGVHWRDWRQLCGVAFLRLDNLACHQLSLSLVPQGLLFAQVTFCDPVI  
 ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSSPSTISPPKGCPR  
 PTTLREASDPATPSNFLPKKTPLEEMTPPPKPPRLYLPQEPTEETPRTKRPHMEPRTR  
 RGPSPASPTRKPPRLQDFRCLAVLGRGHFGKVLVQFKGTGKYAIKALKKQEVLSRDE  
 IESLYCEKRILEAVGCTGHPFLLSLLVCFQTSSEHARFVTEFVPGGLMMQIHEDVFPEPQ  
 ARFYVACVVLGLQFLHEKKIYRDLKLDNLLDAQGLKIADFGLCKEGIGFGDRTSTFC  
 GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPG  
 FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPPFRTTNWQALLARTIQPPFVPTLC  
 GPADLRYFEGETGLPPALTPPAPHSLLTARQQAARDFDFVSEFLEP

SEQ ID NO: 134\_AI021023\_M\_PKNBETA\_M  
 LKWDNLLLLDAQGLKIADFGLCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG  
 LGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPGFLSVQGLEFIQKLLQKCPEKRLGA  
 GEQDAEEIKVQPPFRTTNWQALLARTIQPPFVPTLCGPADLRYFEGETGLPPALTPPAP  
 HSLLTARQQAARDFDFVSEFLEP

SEQ ID NO: 135\_H19102\_H  
 GGNIRGPWARGWKSLLWTGLGTIRSDLEELWELRGHHYHQLHESLKPAPVLVEKPLPEWPVP  
 QFINFLPEFPIRPIRGQQQLKILGLVAKGSFGTVLKVLDCTQKAVFAVKVVPKVVLQR  
 DTVRQCKEEVSIQRQINHPFVHSLGDSWQGRHLFIMCSYSTDLYSLWSAVGCFPEASI  
 RLFAAELVLVLCYLDLGIHRDVKMENILLDERGHLKLTDFGLSRHVPQGAQAYTICGT  
 LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFPVAAERDHSVTHSDSEIPAS  
 LNQGLSLLLHELLCQNPPLHRLRYLHHPVHPFFRGVAFDPELLQKQPVNFVTETQATQPS  
 SAETMPFDDFDCDLESFLLYPIPA

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## FIGURE 1D

SEQ ID NO: 136\_AA476563\_H  
 MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFTLPDGDASRSFNTSESKVEFKAQ  
 DTISRGSDSDSVPVISFKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN  
 IGIIENKLLLEAPDVLCLRLSTEQCQ<sup>~</sup>AHEEKGIEELSDPSGPKSYSITEKHYAQEDPRMLF  
 VAAVDHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTEESLFRICSPLSGANEYIASTDT  
 LKTEEVLLFTDQDDLAKEEPTSLFQORDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS  
 RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILNDRGHIQLTYFSRWSEVEDS  
 CDSDAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP  
 ECVSEEARSLIQQLLQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR

SEQ ID NO: 137\_AA626690\_H  
 MLFPAPQDEPWREMEVFSGGGASSGEVNLKMWDEPMEEGEADSCHDEGVVKEIPITHH  
 VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT  
 KMERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTTEEDVKFYLA  
 ELALALDHLHQLGIVYRDLKPENILLDEIGHIKLTDGFLSKESVDQEKKAYSFCGTVEYM  
 APEVVNRRGHSQSADWWSYGVLMFEMLTGTLPFQKDRNETMNMILKAKLGMPOFLSAEA  
 QSLLRMLFKRNPANRLGSEGVEEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDFTFCF  
 DBEFTAKTPKDSPLPASANAHQLFKGFSFVATSIAEYKITPITSANVLPVQINGNAA  
 QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKIIDKSKRDPSEEIEILMRYGQHPNI  
 ITLKDVFDDGRYVYLVTDLMKGGELLDRILKQKCFSEASDILYVISTVDYLHCQGVV  
 HRDLKPSNILYMDESASADSIRICDFGFAKQLRGENGILLTPCYTANFVAPEVLMQQGYD  
 AACDIWSLGLVLFYTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNISDGAKDLL  
 SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKGAMVATYSALTHKTFQ  
 PVLEPVAASSLAQRRSMKKRTSTGL

SEQ ID NO: 138\_AA215680\_H  
 MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVPDMTKRDYLVDAATQIRLA  
 LERDVSEDYEAAFNHYQNGVDVLLRGIVDPNKERRAEVVKLKITKYLRRAEIIFNCHLQR  
 PLSSGASPSAGFSSLRLRPITLSSAVEQLRGCRVVGVIKVLQVQDPATGGTFVVKSLP  
 RCHMVSRRERTIIPHGVPYMTKLLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL  
 SSGSTQERMKAQLNPHLNLTPARLP SGHAPGQDRIALEPRTSPNLLLAGEAPSTRPQR  
 EAEGEPTARTSTSGSSDLPAKPGGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG  
 RGMDQSCLSADGAGRGCRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLHPGNLLL  
 DQAGHIRLTYFGQWSEVEPQCCGEAVDNLISAPEVGGISELTEACDWWFSGSLLYELLTG  
 MALSQSHPSGIQAHTQLQLPEWLSRPAASLLTELLQFEPTRRRLGMGEGGVSKLKSHPFFS  
 TIQWSKLVG

SEQ ID NO: 139\_SGK\_H  
 MTVKTEAAKGTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKI  
 SQPQEPPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA  
 EVFYAVKVLQKKAILKKKEEKHIMSERVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN  
 GGELFYHLQQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD  
 FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYR  
 NTAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW  
 DDLINKKITPPFNPVSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLG  
 FSYAPPTDSFL

SEQ ID NO: 140\_AA107515\_M  
 MTVKAEAAARSTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM  
 SHPQEPPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA

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## FIGURE 1E

EVFYAVKVLQKKAAILKKKEEKHIMSERVLLKNVKNHPFLVGLHFSFQTADKLYFVLDYIN  
GGELFYHLQORERCFLPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD  
XFQLRRIEHNGTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN  
TAEMYDNILNKPLQLKPNTNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD  
DLINKKITPPFNPVSGPSDLRHFDPFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF  
SYAPPVDSFL

SEQ ID NO: 141\_AA109508\_M  
HLQORERRFLEPRARFYAAEIVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGLCKE  
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLYGLPPFYSDVSQMY  
ENILHQPLQIPGGRTVAACDLLQSLHKKDQORQLGSKADFLEIKNHVFFSPINWDDLYHK  
RLTPPFNPVNTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDD  
ILDC

SEQ ID NO: 142\_AA887783\_H  
MQRDHTMDYKESCPVXIPSSDEHREKKKRFTVYKVLVSVGRSEWFVPRRYAEFDKLYNT  
LKKQFPAXALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMD  
SPKHQSDPSEDEDERSSQKLHSTSQNLNIGPSGNPHAKPTDFDFLKVIGKGSFGKVLAK  
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKNHPFLVGLHYSFOTTEKLYFVL  
DFVNGGEGHVLTDFGLCKEGIAISDTTTFCTPEYLAPEVIRKQPYDNTVDWWCLGAV  
LYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSSILEELLEKDRQNLGAKEDF  
LEIQNHPPFESLSWADLVQKKIPPPFNPVAGPDDIRNFDTAFTEETVPYSVCVSSDYSI  
VNASVLEADDAFVGFSYAPPSDLFL

SEQ ID NO: 143\_R47805\_H  
MAHOTGIHATEELKEFFAKARAGSVRLIKVVIDEQVLVLGASQEPVGRWDQDYDRAVLPL  
LDAQQPCYLLYRLDSQNAQGFELFLAWS PDNSPVRLKMLYAAATRA TVKKEFGGHIKDE  
LFGTVKDDLSFAGYQKHLSSCAAPLTSARELQQIRINEVKTEISVESKHQTLQGLAF  
PLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVHTEPTDVAQLPSRVPRAARYHFFL  
YKHTHEGDPLESVVFYISMPGYKCSIKERMLYSSCKSRLDSVEQDFHLEIAKKIEIGDG  
AELTAFLYDEVHPKQHAFKQAFAPKPGPGGKRGHKRLIRGPGENGDD

SEQ ID NO: 144\_H60215\_H  
MSKLRMKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLAR  
KDGTDDFYQLKILTLEERGDOGIESQEEROGKMLLHTEYSLLSLHTQDGVVHHHGLFQD  
RTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFSDKTADLINLQHYVIKEKRLSERETV  
VIFYDVVRVVEALHQKNIVHRDLKLGNMVLNKRTHRITITNFC LGKHLVSEG DLLKDQRG  
SPAYISPDVLSGRPYRGKPSDMWALGVVLTMLYQGFPPFYDSIPQELFRKIKAAEYTIPE  
DGRVSENTVCLIRKLLVLDPOQLAAADVLEALS AIIASWQSLSSLSGPLQVVPDIDDQM  
SNADSSQEAKVTEEC SQYEFENYMRQQLLLAEKSSIHDTRSWVPKRQFGSAPPVRLGH  
DAQPMTSLDTAILAQRYLRK

SEQ ID NO: 145\_SGK324\_H  
MASTRSIELEHFEERDKRPRPGSRRGAPSSSGGSSSSSGPKGNGLIPSPAHSACSFYRTR  
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV  
RTIYTIDGSRKVTSLDELLEGESYVCASNEPFRKVDYTKNINPNWSVNIKGGSRALAAA  
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKKTAHSFEQVLTDTI TEAIKXASG  
VVKRLCTLDGKQVRVTCVHLPDFFGDDDVFIACGPEKFRYAQDDFVLDHSECRVLKSSYS  
RSSAVKYSKSGKSPGSRRSQISAHGRSSSNVNGGPELDRCISPEGVNGNRCSESSTLLEK  
YKIGKVI GDGNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

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## FIGURE 1F

MLVEEMETATELFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH  
RDIKPENLLVCEYPDGKSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD  
IWAAGVITYILLCGFPFPRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ  
VNVEARCTAGQILSHPWVSDASQENNMQAEVTGKLKQHFNNALPKQNSTTTGVSVMVS  
GRRQVWPDCGAGLEVFEGLSRELPSHGSWCLP

SEQ ID NO: 146\_W30246\_M SGK324\_M  
TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSPEGVNGNRCSESFPILLEKYR  
IGKVIGDGNFAVVKECVDRYTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNIIML  
VEEMETATDLFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHLSLIVHRD  
IKPENLLVCEYPDGKSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW  
AAGVITYILLCGFPFPRSENNLQEDLFDQILAGKLEFPAPYWDNITDSPCVCFRKCL

SEQ ID NO: 147\_AA383293\_H  
PAAKRVVYRNGDPFFPGSQLVVTQRRFPTMEAFICEVTSAVQAPLAVRALYTPCHGHPV  
TNLADLKNRGQYVAAGFERFHKLPYQAFCLSVFRNGDLVSPFFSLKLSQAASQDWETVL  
KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPPALSTRGLLAA  
GNEAHLRSGVGTVAGSPKPLGRKAKKETCLIVTLTKYQQSETSRDQSGFSGVIGVYGA  
PHRRKETAGALEVADDEDQTEEPLDQRAAQIVEQVTCLODFFGDDDDVFIACGPEKFRYA  
QDDFVLDHSRRRLREHQAGFEKLRRTRGEEKEAEKEKKPCMSGRRMTLRDDQPAKLEK  
EPKTRPEENKPERPSGRKPRPMGIIAANVEKHYETGRVIGDGNFAVVKECRHRETRQAYA  
MKIIDKSRLKGKEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAI  
IESVKFPEPDAALMIMDLCKALVHMHDKSIHVRLDKPENLLVQRNEDKSTTLKLADFGLA  
KHVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPFPRSPXXGDQDE  
LFNIIQLGHFEFLPPYWDNISDAKDLVSRLLVVDPPKKRYTAHQVLQHPWIETAGKTNTV  
KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148\_AA197883\_M  
MPTAPVLRPPPPATPAPPAPSRPAPPPIGHRGPCDHSCLKCLSSKISERKLPGPWLPAGR  
GPLEKPVLGPRGAVMPLFSPQSSLHSVRAEHSPLKPRVVTVVKLGQPLRKATLLNRRS  
VQTFEQLLSDISEALGFPRWKNDVRKLFITLKGREKSVSDFFREGDAFIAMGKEPLTLK  
SIQLAMEELYPKNRALALAPHSRVPSRLRSRLPSKLLKGSHRCEAGSYSAMESKAVS  
RHQGTSTVLAPEDKARAQKWVRGKQSEPGGPPSPAATQEETHASGEKHLGVEIEKTS  
GEIVRCEKCKRERELQLGLQREPCPLGTSELDLGRAQKRDSEKLVRTKSCRPSKAKFTD  
GEEGWKGDSHRGSPRDPPQEMRRPNSNSDKKEIRGSESQDSYPQAPKAQKDFVEGPPAV  
EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPQLPRTRGEEKQAEHEKKPGGLGERRAPE  
KESKRKLEEKRPERSGRKPRPKGIIISADVEKHYDIGGVI GDGNFATVKECRHRETKQAY  
AMKMIDKSQKKGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYLIMEYVQGGDLFDA  
IVENVKFPEPEAAVMITDLCKAFVHMHDKNIVHRDVKPENLLVQRNEDKSTTLKLADFG  
AKYVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPFPRSPERDQDE  
LFNIIQVQGFEFLSPYWDNISDAKDLVRNLLVDPKKRYTAEQVLQHPWIEMVGHTNTG  
NSQKEESPSNLGHFQSQHKKVAEQMP

SEQ ID NO: 149\_DRAG2\_H  
MSRRRFDCRSISGLLTTPQIPIKMENFNFFYILTSKELGRGKFAVVRQCISKSTGQEYA  
AKFLKKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS  
LCLPELAEMVSENDVIRLIKQILEGVYYLHQNINIVHLDLKPONILLSSIIYPLGDIKIVDF  
GMSRKIGHACELREIMGTPEYLAPEILNYDPITTTATDMWNIGIIAYMLLTHTSPFVGEDN  
QETYLNI SQVNDYSEETFSSVSQLATDFIQSLLVKNPEKRPTAEICLSHSWLQQWDFEN

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## FIGURE 1G

LFHPEETSSSSQTQDHSVRSSSEDKTSKSSCNGTCGDREDKENI PEDSSMVSKRFRFDDSL  
PNPHELVSDDL

SEQ ID NO: 150\_W44160\_M DRAK2\_M  
MSRRRFDCRSVSGLLTTTPQTPIKTENFNNFYTLTPKELGRGKFAVVRQCISKSTGQEYA  
AKSLKKRRRGQDCRAEILHEIAVLELARSCHVINLHEVYENATEIILVLEYAAGGEIFN  
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNINIVHLDLKPQNILLSSIIYPLGDIKIVDF  
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN  
QETYNISQVNVVDYSEEMFSSVSQATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS  
LFHPEETSGSSQIQDLTLRSSEKTSKSSCNGSCGAREDKENI PEDGSLVSKRFRFDDSL  
PSPHELVPDLFC

SEQ ID NO: 151\_H01248\_H, DRAK1\_H  
MIPLEKPGSGGSSPGATSGSGRAGRLSGPCRPPPPQARGLLTEIRAVVRTEPFQDGYS  
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRKGQDCRMEIIEIAVLELAQDNPW  
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR  
DVVHLDLKPQNILLTSESPGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI  
SMATDMWSIGVLTIVMLTGISPFLGNDKQETFLNISQMNLSYSEEFVDLSESVDVFIRT  
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDDTKSE  
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAI SKRKFEEPLLQEIPGEFIY

SEQ ID NO: 152\_AA021445\_H  
MPARIGYYEIDRTIGKGNFAVVKRATHLVTKAKVAIKIIDKTQLDEENLKKIFREVQIMK  
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFKQIVTAVYF  
CHCRNI VHRDLKAENLLLDANLNKIADFGFSNFTPGQLLKTWCGSPPYAAPELFEGKE  
YDGPKVDIWSLGVVLYVLVCGALPFDGSTLQNLRLARVLSGKFRI PFFMSTECEHLIRHML  
VLDPNKRLSMEQICKHKWMKLGADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL  
DKEQTLQSLRSDAYDHYSIYSLCDRHKRHKTLRLGALPSMPRALAFQAPVNIQAEQAG  
TAMNISVPQVQLINPENQIVEPDGTLNLDSEGEEPSPEALVRYLSMRHTVGVADPRTE  
VMEDLQKLLPGFPGVNPQAPFLQVAPNVNFMHNLPMQNLQPTGQLEYKEQSLQPPTLQ  
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPDQ  
EAVQRYLANRSKRHTLAMTNPTAEI PPDLQRLGQQPFRSRVWPPHLVPDQHRSTYKDSN  
TLHLPTERFSPVRRFSDGAASIQAFAHLEKMGNNSSIKQLQCECEQLQKMYGGQIDERT  
LEKTQQQHMLYQEQHHQILQQQIQDSICPPQSPPLQAACENQPALLTHQLQLRIQPS  
SPPPNHPNNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSIIFQQQPPENCSSPPN  
VALTCLGMQQAQSQQVTIQVQEPVDMLSNMPGTAAGSSGRGISISPSAGQMOMQHRTNL  
MATLSYGHRPLSKQLSADSAEAHSLNVNRFSPANYDQAHLPPLFSDQSRGSPSSYSPST  
GVGFSPTQALKVPLDQFPTFPFSAHQPPHYTTSAQQALLSPTPPDYTRHQQVPHILQ  
GLLSRPHSLTGHSIDIRLPTEFAQLIKRQQQQRQQQQQQQQQEQELFRHMNQGDAGSL  
APSLGGQSMTERQALSQNADSYHHHTSPQHLLQIRAEQCVSQASSPTPPHYAHQPALM  
HSESMEEDCSCEGAKDGFQDSKSSSTLTGCHDSPLLLSTGGPGDPESLLGTVSHAQELG  
IHPYGHQPTAAFSKNKVPSPREPIGNMCDRSSPGQAVELPDHNLGYPARPSVHEHHRPR  
ALQRHHTIQNSDDAYVQLDNLPGMSLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE  
CGASLGGHEHPDLSDGSLNSSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153\_2R22-5-11\_H  
MTAVYMNGGGLVNPYARWDRRDSVESGCQTESKEGEEGQPRQLTPFEKLTQDMSQDEK  
VVREITLGKRIGFYRIRGEIGSGNFSQVKLGHSITKEKVAIKILDKTKLDQKTQRLLSR  
EISSMEKLHHPNIIRLYEVVETLSKLHLMVMEYAGGGELFGKISTEGKLSEPESKLIFSQI  
VSAVKHMHENQIIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

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## FIGURE 1H

LFRDEHYIGIYVDI WALGVLLYFMVTGTMPFRAETVAKLKKSILEGTYSVPPHVSEPCHR  
LIRGVLQIQPTERYGIDCIMNDEWMQGVPTPLEPFQLDPKHLSETSTLKEEENEVKST  
LEHLGITEEHIRNNQGRDARSSITGVYRIILHRVQRKKALESVPMMLPDPKERDLKKGS  
RVYRGIRHTSKFCSIL

SEQ ID NO: 154\_R31237\_1\_H, AAC33487  
MSTRTPLTVNERTDENTHTSHGDRQEVTSRTSRSGARCRNSIASCADQPHIGNYRLLK  
TIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPTSLQKLFREVRIMKILNHPNIVKLFE  
VIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK  
AENLLLDADMNIAIDFGFSNEFTVGGKLDTCGSPPYAAPLFGQKKYDGPVDVWSLG  
VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFVLNPIKRGTLQ  
IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESLSMKMYDEITAT  
YLLLGKRSSELDASDSSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQSVSSSQKQRRYS  
HAGPAIPSVVAYPKRSQTSTADGDLKEDGISSRKSSGSAVGGKGIAPASPM LGNASPNK  
ADIPERKKSSTVPSSNTASGGMTRRNTYVCSERTTADRHSVIQNGKENSTIPDQRTFVAS  
THSISAAATPDRI RFPRTASRSTFHGQPRERRTATYNGPPASPSLSHEATPLSOTRSRG  
STNLFSKLTSLKTRSRNVSAEQKDENEAKPRSLRFTWSMKTTSMDPGDMMREIRKVL  
ANNCDYEQRRERFLLFCVHGDGHAENLVQWEMEVCKLPRLSLNGVRFKRI SGTSLAFKNIA  
SKIANELKL

SEQ ID NO: 155\_W90839\_M  
KGPSWSSRSLGARCRNSIASCPEEQPHVGNRYRLLRTIGKGNFAKVKLARHILTGREVAIK  
IIDKTQLNPSSLQKLFREVRIMKGLNHPNIVKLFEVIETEKTLYLIMEYASAGEVFDYLV  
SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLLDAAEANIADFGFSNEFTL  
GSKLDTFCGSPPYAAPLFGQKKYDGPVDIWSLGVILYTLVSGSLPFDGHNKELRERV  
LRGKYRVPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEELKPDTELKEE  
RMPGRKASAVGSGSRGLPPSSPMVSSAHNPNAEIPERRKDTSTPNNLPPSMMTRRN  
TYVCTERPGSERPSLLPNGKENS SGT SRVPPASPSHSLAPPSGERSRLARGSTIRSTFH  
GGQVRDRRAGSGGGVQNGPPASPTLAHEAAPLPSGRPRPTTNLFTKLTSLKTRRVTD  
PERIGGPEVTSCHLPWDKTETAPRLLRFPWSVKLTSSRPS

SEQ ID NO: 156\_406786.5\_H  
MEVGGLTVFEEDQRCLSQLPLPVSAEGPAAQTAEPSRSFSSAHRHLSRRNGLSRLCQS  
RTALSEDRWSSYCLSSLAQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSSGWSS  
PLLPAVPCNPNAIFTVDKTTTEILVANDKACGLLGYSSQDLIGQKLTQFFLRSDSDVE  
ALSEEHEADGHAAVFGTVVDIITRSGEKI PVSVWMKRMQRERRCCVVVLEPVERVST  
WVAFQSDGTITSCDSLFAHLHGYVSGEDVAGQHITDLIPSVQLPPSGQHIKPNLKIORSV  
GRARDGTTFFLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI  
NHSFALTFLGYGKTELLGKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDVGNESGCGER  
TLDPWQGGQDPAEGGQDPRINVVLGGHVVRDEIRKLMESQDIFTGTQTELIAGGQLLSC  
LSPQAPAGVDNVPEGSLPVHGEQALPKDQOITAGREEPVAIESPGQDLLGESRSEPDV  
KPFASCEDSEAPVPAEDGGSDAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ  
LAGGSLLMHCPCYGSEWGLWWSQDLAPSPSGMAGLSFGTPTLDEPWLGVENDREELQTC  
LIKEQLSQLSLAGALDVPHAEVLPTECQAVTAPVSSCDLGGRLCGGCTGSSSACYALAT  
DLPGGLEAVEAQEVDVNSFSWNKELFFSDQTDQTSNCS CATSELRETPSSSLAVGSDPD  
VGSLOEQGSCVLDRELLLTGTCDVLDGQGRRFRESCVGHDPTEPLEVCLVSEHYAASD  
RESPGHVPSTLDAGPEDTCSAEPEPRLNVQVTSTPVI VMRGAAGLQREIQEGAYSGSCYH  
RDGLRLSIQFEVRRVELQGPTPLFCCWLKDLLHSQRDSAARTRFLASLPGSTHSTAAE  
LTGPSLVEVLRARPWFEEPPKAVEGLEGLAACEGEYSQKYSTMSPLGSGAFGVWTAVDKG  
KNKEVVVKFIKKEKVLEDCWIEDPKLGKVTLTAIILSRVEHANI KVLDFENQGGFFQLV



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## FIGURE 11

MEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDIHRDIKDN  
 IVIAEDFTIKLIDFGSAAYLERGKLFYTFCTIEYCAPEVLMGNPYRGPELEMWSLGVTL  
 YTLVFEENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQPVPERRTTLEKLVTDWPVWTO  
 PVLADYTWEVFRVKNKPESGVLASASLEMGNRSLSDVAQAQELCGGPVPGAPNGQGC  
 HPGDPRLLTS

SEQ ID NO: 157\_AA544838\_M 406786\_M  
 TRPHPCLEPLASFIHQVLSAVGYLHSGQIIHRDIKDNIVIAEDFTIKLIDFGSAAYL  
 ERGKLFYTFCTIEYCAPEVLIGNPYRGPELEMWSLGVTLTYTLIFEENPFCEVEETMEAV  
 IHPFLVSQELMSLLSGLLQPCPEQRTTLEKLVIRDPWVTQPVNLASYTWEVCRNQPES  
 GLLSAASLEIGSRSPSEMAQREGLCGPPAPRETRGDQHCLHLKDPSPVPS

SEQ ID NO: 158\_AA785735\_H  
 MVMADGPRHLQGRPVVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQOLDAVN  
 LEKIYREVQIMKMLDHPHIIKLYQVMTKSMYLVTEYAKNGEIDYLANHGRNLNESEAR  
 RKFWQILSAVDYCHGRKIVHRDLKAENLLDNNMNIKIADFGFGNFFKSGELLATWCGSP  
 PYAAPEVFEGQQYEGPQLDIWSMGVVLVLCGALPFDGPTLPILRQVLEGRFRIPYFM  
 SEDCEHLIRMLVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV  
 LRLMHSGLIDQOKXIESLQNKSYNHFAAIYFLLVERLKSRRSFPVEQRLDGRQRRPSTI  
 AEQTVAKAQTVGLPVTMHSNMRLLRSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT  
 PKVNGCLLDVPPVLRKGCQSLPSNMETSIDEGLETEGEAEEDPAHAFAEFQSTRSGQ  
 RRHTLSEVTNQLVVMGAGKIFSMNDSPLSDSVSEYDMGSVQRDNLNFDENPSLKDIML  
 ANQPSRMTSPFISLRPTNPAMQALSSQKREVNRSVPVSFREGRRASDTSLTQGIVAFRQ  
 HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST  
 LPASVHPQLSPRQSLQYLOHRLQKPSLLSKAONTQOLYCKEPPRSLEQQQLQEHRLQOK  
 RLFLQKQSQLQAYFNQMQUIAESSYPQPSQQLPLPRQETPPPSQQAAPPFLSTQPLSPVLEP  
 SSEQMQYSPFLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQQPPPPPPPPPPRQPGAAPA  
 PLQFSYQTCELPSAASPAPDYPTPCQYPVDGAQQSDLTGPDCPRSPGLQEAPSSYDPLAL  
 SELPGLFDCEMLDAVDPQHNGYVLVN

SEQ ID NO: 159\_AA207220\_H  
 MESLVFARRSGPTPSAAELARPLAELIKSPKPLMKKQAVKRHHHKHNLRRHYEFLETGLG  
 KGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIEHVEFE  
 NSSKIVIVMEYASRGDLYDIYSERQQLSEREARHFFRQIVSAVHYCHQNRVVRDLKLEN  
 ILLDANGNIKIADFGLSNLYHQGKFLQTFGSPLYASPEIVNGKPYTGPEVDSWSLGVLL  
 YILVHGTMPFDGHDHKLIVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS  
 HWWVNWGYATRVGEQAPHEGGHGPSDSARASMDWLRRSSRPLENGAKVCSFFKQHAP  
 GGGSTTPGLERQHSLSKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPGKILKKKVSASA  
 EGVQEDPPELSPIPASPGQAAPLLPKKGILKKPRQRESGYSSPEPSESSELDDAGDVV  
 SGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPLARSRP  
 SGAVSEDSILSSESFQDLDLPERLPEPPLRGCVSDNLTGLEEPPSEGGPSCLRRWRQDP  
 LGDSCFSLTDCQEVATYRQALRVCSKLT

SEQ ID NO: 160\_AA426580\_H, MAK\_V\_H  
 MPAAAGDGLLGEPAAPGGGGGAEDAAAPAAACEGSFLPAWVSGVPRERLRDFQHHKRVGN  
 YLIGSRKLGECSFAKVREGLHVLTKGKVAIKVIDKKRAKDTYVTKNLRREGQIQQMIRH  
 PNITQLLDILETENSYYLVMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA  
 GVVRDLKIEENLLDDENNIKLIDFGLSNACAGILGYSDPFSTQCGSPAYAAPELLARKKY  
 GPKIDVWSIGVNMAMLTGTLPFTVEPFLRALYQKMVDKEMNPLPTQLSTGAISFLRSL  
 LEPPDPVKRPNIQQALANRWLNENYTGKVPNCVTYPNRISEDLSPSVVLHMTEKLGKNS



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## FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLCKTRLYQIEKYRAPKESYEA  
SLDTWTRDLEFHAVQDKKPKKEQKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA  
LLKDRKASKSSFPDKDSFGCRNIFRKTSDSNVASSSMEFIPVPPPTPRIVKKPEPHQP  
GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHHYRILNSPVSLARRNSSERTLS  
PGLPSGMSPLHTPLHPTLVSFHEDKNSPPKEEGLCCPPVPVPSNGPMQPLGSPNCVKSR  
GRFPMGIGQMLRKRHQSLSQPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161\_Z36720\_H  
MDTKLNLNEKVDQLLHFQEDVTEKLQSMCRDMGHLERGLHRLEASRAPGPGGADGVPHI  
DTQAGWPEVLELVAMQDAAQHGARLEALFRMVAAVDRAIALVGATFQKSKVADFLMQG  
RVPWRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQDKGELSAEQGIWATLMTLV  
IMVTAANKERVEEEGGKPKHVLSTSGVQSDAREPGEESQKADVLEGTAERLPPIRASGLG  
ADPAQAVVSPGQGDGVPGPAQAFPGHLPLPTKVEAKAPETPSENLRGTGLELAPAGRVNV  
VSPSLEVAPGAGQGASSRPDPEPLEEGTRLTGPGPGQCPGPPGLPAQARATHSGGETTP  
RAALLKGAVAPGFSRRDLVFPSIFCACLGISIHQEMDTPGEMLMTGRGSLGPTLTTEAP  
AAAQPGKQGPPTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEEQRAGAEPG  
TRPSLARSDDNDHEVGALGLQQKSPGAGNPEPEQDCAARAPVRAEAVRRMPPGAEAGSV  
VLDDSPAPPAPFEHRVVSVKETSISAGYEVQCHEVLGGGRFGQVHRCTEKSTGLPLAAKI  
IKVKSADREDVKNEINIMNQLSHVNLIQLYDAFESKHSCTLVMEYVDGGELFDRITDEK  
YHTELDDVVLFTROIPEGVHYLHQHYILHLDLKPENILCVNQTGHQIKIIDFGLARRYKP  
REKLKVNFGTPEFLAPEVVNYEFVSPFTDMWSVGVI TYMLLSGLSPFLGETDAETMNFIV  
NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCRMSATQCLKHEWLNLPKASRSKTRLK  
SQLLLQKYIAQRKWKKHFFYVVTAANRLRKFTSP

SEQ ID NO: 162\_SGK088\_H  
GEMALFECLVAGPTDVEVDWLCRGRLLPALLKCKMHFDGRKCKLLLTSVHEDDSGVYTC  
KLSTAKDELTC SARLTVRPSLAPLFTRLLEDVEVLEGRAARFDCKISGTPPPVTWTHFG  
CPMEESLENRLRQDGLHSLHIAHVGEDEGLYAVSAVNTHGQAHCSAQLYVEEPRTAAS  
GPSSKLEKMPISIPPEEQGELERLSIPDFLRPLQDLEVGLAKEAMLECQVTGLPYPTISW  
FHNGHRIQSSDDRMTQYRDVHRLVFPVAGPQHAGVYKSVIANKLGAACYAHLVYTDVV  
PGPPDGAPQVAVTGRMVTLTWNPPRSLDMAIDPDSLTYTVQHQLGSDQWALTGLRE  
PGWAATGLRKGVQHI FRVLSTTVKSSSKSPSEPVLLEHGPTLEEAPAMLDKPDIVYV  
VEGQPASVTVTFNHVEAQVVRSCRGALLEARAGVYELS QPDDQYCLRICRVSRRDMGA  
LTCTARNRHGTQTC SVTLELAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKD  
EVLLTESSHVSFVYEENEC SLVVLSTGAQDGGVYTCTAQN LAGEVSCKAELAVHSAQTAM  
EVEGVGEDEDHRRRLSDFYDIHQEIGRGAFSYLRRIVERSSGLEFAAKFI PSQAKPKAS  
ARREARLLARLQHDCVLYFHEAFERRRGLVIVTELCTEELLERIAKPTVCESEIRAYMR  
QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRI CDFGNAQELTPGEPQYCYGTF  
EFVAPEIVNQSPVSGVTDIWPVGVAFLCLTGISPFVGENDRITLMNIRNYNVAFEETTF  
LSLSREARGFLIKVLVQDRLRPTAETLEHPWFKTQAKGAEVSTDHLKFLSRRRWQRSQ  
ISYKCHLVLRPIPELLRAPPERVWVTMPRRPPPSGGLSSSSDSEEELEELPSVPRPLQP  
EFGSRVSLTDIPTEDALGTPETGAATPMDWQEQGRAPSQDQEA PSPEALPSPGQEPAA  
GASPRRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEG  
EYAQRQLQALRQRLLRGGPEDGKVSGLRGP LLES LGGRARDPRMARAASSEAAPHQPPLE  
NRGLQKSSSFQGEAEPRGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQPSSPARP  
SAPKPSTPKSAEPSATTPSDAPQPPAPQPAQDKAPEPRPEPVRSKPA PPAQALQTLALP  
LTPYAQIIQSLQLSGHAQGPSQGPAAAPPSEPKPHA AVFARVASPPPGAPEKRVPSAGGPP  
VLAEKARVPTVPPRPGSSLSSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG  
PFRGAEEEDGIYRPSAGTPELVRRPERSRSVQDLRAVGEPGLVRLSLSLSQRLRRTF  
PAQRHPAWEARGGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQSRGSSSEDSSGGAS

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## FIGURE 1K

GRSTPLFGRLRRATSEGESLRRRLGLPHNQLAAQAGATTPSAESLGSEASATSGSSAPGES  
 RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPFVFIKLKDQVLLEGEAA  
 TLLCLPAACPAPHISWMKDKSLRSEPSVIVSCKDGRQLLSIPRAGKRHAGLYECSATN  
 VLGSITSSCTVAVARVPGKLAPPEVTQTYQDTALVLWKPGDSRAPCTYTLERRVDGESVW  
 HPVSSGIPDCYINVTHLPVGVTVRFRVACANRAGQGPFNSSEKVFVRGTQDSSAVPSAA  
 HQEAPVTSRPARARPPDSPTS LAPPLAPAAPTPPSVTVSPSSPPTPPSQALSSLKAVGPP  
 PQTPPRRHRGLQAARPAEPTLPSTHVTTPSEP KPFVLDTGTPIPASTPQGVKPVSSSTPVY  
 VVTSFVSAPPAPEPPAPEPPPEPTKVTVQSLSPAKEVVSSPGSSPRSSPRPEGTTLRQGP  
 PQKPYTFLEEKARGFRGVVRACRENATGRTFVAKIVPYAAEGKPRVLQEYEVLRTLHHER  
 IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFRYSEDDVATYMVQLLOGLDYLHGHV  
 LHLDIKPDNLLLAPDNALKIVDFGSAQPPYNPQALRPLGHRTGTLEFMAPEMVKGEPIGSA  
 TDIWAGVLTYYIMLSGRSPFYEPDPQETEARIVGGRFADFOLYPNTSQSATLFLRKVLSV  
 HPWSRPSLQDCLAHPWLQDAYLMKLRROTTLTFTTNRLKEFLGEQRRRRAEAAATRHKVLLR  
 SYPGGP

SEQ ID NO: 163\_AA542015\_M SGK088\_M  
 ATDIWAGVLTYYIMLSGYSPFYEPDPQETEARIVGGRFADFOLYPNTSQSATLFLRKVLS  
 VHPWSRPSLQDCLAHPWLQDAYLMKLRROTTLTFTTNRLKEFLGEQRRRRAEAAATRHKVLL  
 RSYPGSP

SEQ ID NO: 164\_R19772\_H  
 MKGGDRAYTRGPSLGWLFKCCCCFPCTDAYSHSSSENGGKSESVANLQAQPSLNFHSS  
 PGKRSTNTLKKWLTSPVRLNSGKADGNIKKQKKVRDGRKSF DLGSPKPGDETTPQGDS  
 ADESKKGWGEDEPDEESHTPLPPPMKIFDNDPTQDEMSSSLAARQASTEVP TAADLVNA  
 IEKLVKNKLSLEGSSYRGLKDPAGCLNEGMAPPTPPKNPEEEQKAKALGRMFVNLV  
 QTEKDYVDLGI VVEGFMKRIEEKGVPEMDRGDKIVFGNIHQIYDWHKDFFLAELEKCI  
 QEQDRLAQLFIKHERKLHIYVWYQCNKPRSEYIVAEYDAYFEEVKQEI NRRLTSLDFLIK  
 PIQRITKYQLLLKDFLYSEKAGLECS DIEKAVELMCLVPKRCNDMMNLGRLOGFEGTTLT  
 AQGKLLQODTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGS LTPGYMFKRSIKMN  
 YLVLEENVNDNDPCKFALMNRETSE RVVLQANADIQQA WVDINQVLETQRDFLNLQSP  
 IEYQRKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPPLPPLKISTNSGSP  
 GFEYHQPGDKFEASKNDLGCGNGTSSMAVIKDYYALKENEICVSQGEVVQVLAVNQNM  
 LVYQPASDHSPAAEGWVPGSILAPLT KATAAESDGS IKKSCSWHTLRMRKRAEVENTGK  
 NEATGPRPKDILGNKVS VKETNSSESECDLDPNTSM EILNPNFIQEVAFELVPLVD  
 VTCLLGDTVILQCKVCGRPKPTITWKGPDQNI LDTDNSSATYTVSSCDSGEITLKI CNLM  
 PQDSGIYTCIATNDHGTST SATVKVQGVPAAPNRPIAQERSCTSVILRWLPPSSTGNCT  
 ISGYTVEYREEGSQIWQQSVASTLD TYLVIEDLSPGCPYQFRVSASNPWGISLPSEPSEF  
 VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKCKIHKATR KDVAVKFVNKKM  
 KKKEQAHEAALLQHLQHPQYITLHDTYESPTS YILILELMDDGRLLDYL MNHDELMEEK  
 VAFYIRDIMEALQYLHNCRV AHLDIKPENLLIDLRIPVPRVKLIDLEDAVQISGHFHIH  
 LLGNPEFAAPEVIQGIPVSLGTDIWSIGVLT YVMSGVSPFLDESKEETCINVC RVDFS  
 PHEYFCGVSNAARDFINVLQEDFRRRPTAATCLQHPWLQPHNGSYSKIPLDTSRLACFI  
 ERRKHQNDVRPIPNVKS YIVNRVNQGT

SEQ ID NO: 165\_5R72\_8\_2\_H  
 MADSGLDKKSTKCPDCSSASQKDVLCVCSSKTRVPPVLV VEMSQTSSIGSAESLISLERK  
 KEKNINRDISRKDLPSRTSNVERKASQQQWGRGNFTEGKVPHIRIENGAAIEE IYTFGR  
 ILGKGSFGIVIEATDKETETKWA IKKVNEKAGSSAVKLLEREVNILKSVKHEHIHLEQ  
 VFETPKMYLVMELCEDGELKEILDRKGHFSENETRWIIQSLASAIAYLHNNDIVHRDLK  
 LENIMVKSSLIDNNEINLNIKVTD FGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

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## FIGURE 1L

SQOCDIWSIGVVMYMLLRGEPPFLASSEAKLFELIRKGELHFENAVVNSISDCAKSVLKQ  
LMKVDPAHRITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTEKNKPS  
TEEKLKSYQPWGNVPETNYTSDEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE  
IKGEMKTPVTPSQGTATKYPKSGALSRTKKKL

SEQ ID NO: 166\_SGK309\_H  
MQCLAAALKDETMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTREN  
ALKVESAQQPKQVLKMEVAVLKKLQSGGLGQGDGKEEMMKPGAKRGKDHVCRFIGGRNE  
KFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGLHRDIKPSNF  
AMGLPSTYRKCYMLDFGLARQYTNNTGDVPRPNVAGFRGTVRYASVNAHKNRMRHD  
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMKEKEYEHRMLLKHPSEFHLFLDHIASLDY  
FTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPPAEHPADGSHVWG  
GQCDASAWGPAPGEHRGCATGRAPEXPECTPNSAREALXGAGPQSPPCPPPRGSXGXSL  
GGDRCQPEQTPDQHRQSNCRQGEGRGWPFLLSPPIPSLVPLPCSSXAPCPPPIISLLARPLF  
PVPSPALASLCLPSSSSSVSFTLRRPSA

SEQ ID NO: 167\_AA234451\_H  
MSGGGEQLDILSVGILVKERWKVLRKIGGGGFGEIYDALDMLTRENVALKVESAQQPKQV  
LKMEVAVLKKLQGDHVCFIGGRNDRFNYVVMQLQGRNLADLRRSQSRGTFTISTTLR  
LGRQILESIESIHSVGSXHRDIKPSNFAMGRFPSTCRKCYMLDFGLARQFTNSCGDVRRP  
RAVAGFRGTVRYASINAHNRMRGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE  
RYDHRMLKHLPPFESIFLDHISSLDYFTKPDYQLTSVFDNSIKTFGVIESDPFDWEKT  
GNDGSLTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP  
VGVSPDKLPGLHPRPQEKDVWEEMDANKNKLKLGICKAATEEENSHGQANGLLNAPSL  
GSPIRVRSEITQPRDIPLVRLRSIHSFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168\_AA435956\_H  
TFTIFFEMTVFDLEAKSARGGSNLLMDSVSSFQLFMFQLLRGLAYIHHQHVLRDLKPQN  
LLISHLGELKLADFGGLARAKSIPSQTYSSVVTLWYRPPDALLGATEYSSSELDIWGAGCI  
FIEMFQGGQLPFGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPWFPLPTPRSLHV  
VWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV  
RLKPEMCDLLASYQKGHHPAQFSKCW

SEQ ID NO: 169\_AA626859\_H  
NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIKICDFGFAQILIPGD  
AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR  
TLGKLI PRHQSIKSNFGFFHGISIPEPEDMETLEEKFSVHPVALNFMKGCLKMNPDRL  
TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQONQLLPLIPGSHISPTPDGRKQVLQK  
FDHLPNI

SEQ ID NO: 170\_AA061797\_M  
KIALREIRMLKLKHPNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVSDGVKSV  
LWQTLQALNFCHKHNCIHRDVKPENILITKQGMKICDFGFARILIPGDAYTDYVATRWY  
RAPELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLI PRHQ  
IFRSNQFFRGISIPEDMETLEEKFSNVQPVALSFMKGCLKMNPDRLTCAQLLDSAYF  
ESFQEDQMKRKARSEGRSRRRQONQLLPLIPGSHISPTPDGRKQVVLKFDHLPNI

SEQ ID NO: 171\_AA397553\_H  
MPNSERHGGKKGSGGASGTLQPSGGGSSNSRERHRLVSKHKRHSKHSKMDGLVTPEA  
ASLGTVIKPLVEYDDISSDSTFSDDMAFKLDRRENDERRGSDRSRLHKHRHHQHRRSR

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## FIGURE 1M

DLLKAKQTEKEKSQEVSSKSGSMKDRISGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH  
KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSDDSSKQDDSPSGA  
SYGQDYDLSPSRSHTSNNYDSYKKSPGSTSRQSVSPPYKEPSAYQSSTRSPSPYSRRQR  
SVSPYSKKRSSSYERSGSGRSPSPYGRRRSSSPFLSKRSLRSPLPSRKSMKSRSRSP  
AYSRHSSSSHKKRSSSRSRHSSI SPVRLPLNSSLGAELSRKKKRAAAAAAKMDGKES  
KGSFVFLPRKENSSVEAKDSGLESKKLPRSVKLEKSAPDTELNVNTHLNTVKNSSDTGK  
VKLDENSEKHLVKDLKAQGTRDSKPIALKEEIVTPKETETSEKETPPPLPTIASPPPPPLP  
TTTPPPQTPPLPLPPIPALPQQPPLPPSQPAFSQVPASSTSTLPPSTHKTSAVSSQAN  
SQPPVQVSVKTQVSVTAAI PHLKTSTLPLPLPPLPGGDDMDSPKETLPSKPVKKEKEQ  
RTRHLLTDLPLPELPGGDLSPDSEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG  
KRCVDKFDIIGIIGEGTYGQVYKARDKDTGELVALKKVRLDNEKEGFPI TAIREIKILRQ  
LIHRSVVMKEIVTDKQDALDFKKDKGAFYLVFEYMDHDLMLLESGLVHFSEDHIKFSM  
KOLMEGLECHKKNFLHRDIKCSNILLNNSGQIKLADFGARLYNSEESRPTNKVITLW  
YRPPPELLLGEERYTPAIDVWSCGICLGELFTKKPIFQANLELAQLELISRLCGSPCPAVW  
PDVIKLPYFNTMKPKQYRRRLREEFSFIPSAALDLDHMLTLDPSKRCCTAEQTLQSDFL  
KDVELSKMAPDPLPHWQDCHELWSKKRRRQRQSGVVVEPPPSKTSRKETTSGTSTEPVK  
NSSPAPPQPAPGKVESGAGDAIGLADITQQLNQSELAVLLNLLQSOTDLSIPQMAQLLNI  
HSNPEMQQLEALNQSISALTEATSQQQDSETMAPEESLKEAPSAPVILPSAEQMTLEAS  
STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPQGPRTPTMPQEEAAACPPHIL  
PPEKRPPEPPGPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPPGHLPHHEH  
QALRPMEYSTRPRPNRTYGNTDGPETGFSIDTDERNSGPALTESLVQTLVKNRTFSGSL  
SHLGESSYQGTGSVQFPDQDLRFARVPLALHPVVGQPFLLKAEGSSNSVVAETKLQNY  
GELGP GTTGASSSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGRGRGVPI

SEQ ID NO: 172\_AA789239\_H  
MEMYETLGKVGEGSYGTVMKCKHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE  
NLVNLIEVFRQKKIHLVFEFIDHTVLDLQHYCHGLESKRLRKYLFIQLRAIDYLHSNN  
VIIHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYTDYVATRWYRAPELVKDTSYG  
KYVPVDI WALGCMIIEMATGNPYLPSSSDLDLLHKIVLVKXFMPELKAKLLQEAKVNSLI  
KPKESSENELRKDERKTVYTNLLSSSVLGKEIEKEKKPKEIKVRVIVKVGGRGDI SEP  
KKKEYEGGLGQQDANENVHPMSPDTKLVTI EPPNPINPSTNCNGLKENPHCGGSVTMPPI  
NLTNSNLMAANLSSNLFHPSVRLTERAKKRTSSQSISQVMPNSRQEDPGPIQSQMEKGI  
FNERTGHSDQMANENKRKLNFSDRKEFHFPPELPVTIQSKDTKGMEVKQIKMLKRESKK  
TESSKIPTLLNVDQNEKQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173\_AA124976\_M  
LADIVHACLQIDPAERTSSTDLLRHDFYTRDGFIEKFIPELRAKLLQEAKVNSFIKPKEN  
FKENEPVRDEKKSFTNTLLYGNPSLYGKEVDRDKRAKELKVRVIAKGGKGDPDQKKP  
EYEGDHRQOGTADDTQPSLDKKPSVLELTNPLNPSNSDGVKEDPHAGGCMIMPPINLT  
SSNLLAANLSSNLSHPNSRLTERTKKRTSSQITIGQTLNSRQEDTGPTQVQTEKGAFNE  
RTGQNDQISSGNKRKLNF PKCDRKEFHFPPELPFTVQAKEMKGMVKQIKVLKRESKTTDS  
SKIPTLLSMDPNQEKQEGGDGDCEGKNLKRNRFFFSR

SEQ ID NO: 174\_AA575635\_M CCRK\_M  
SASGOLKIADFGLARVFS PDGGRLYTHQVATRWYRAPELLYGARQYDQGVLDLWAVGCIMG  
ELLNGSPLFP GENDIEQLCCVLRILGTPSPRVWPEITELPDYNKISFEEQAPVPLEEVL P  
DASPQALDLLGQFLLYPPRQRIAASQALLHQYFFTA PLPAHPSELPIPQRPGGPAPKAHP  
GPPHVHDFHVDRIEESLLNPELIRPFIPEG

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## FIGURE 1N

SEQ ID NO: 175\_AA631990\_H  
MITSISTEKSNGTHYPMITTLQYYRGRGGKTAVWRHFS AEGPFAFAEMRHSKRTHCPDW  
DSRESWGHESYRGSHKRKRSHSSTQENRHCKPHHQF KESDCHYLEARSLNERDYRDRRY  
VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNHRHCSSHQSRSEXETV  
DTLGEAFAFGKVV ECI DHGMDGMHVAVKI VKNVGRYREAAARSEIQVLEHLNSTDPNSVFR  
VQMLEWFDHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRMAYQIQSINFLHNNKL  
THTDLKPENILFVKSDYVVKYNSKMKRDERTLKN TDIKVDFGSATYDDEHSTLVSTRH  
YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPOHMIQ  
KTRKRKYFHNNQLDWEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQ  
RITLDEALQHPFFDLLKKK

SEQ ID NO: 176\_AA557536\_H  
MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDLSRQERNWPSWA  
PEHSPSWPSSRLRLSPQEFGDHPNII SLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGG  
LQDVHVRISIFYQLLRATRFLHSGHVVRDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG  
PEDQAVTEYVATRWYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT  
STLHQLELILETI PPPSEEXRPRQTL DALLPPDTSPEALDLLRLLVFAPDKRLSATQAL  
QHPYVQRFHCPSEDEWAREADVPRPRAHEGVQLSVPEYRSRVYQMI LECGGSSGTSREKGP  
GVSPSQAHLLHKPRADPQLPSRTPVQGP RP PQSSPGHDP AEHES PRAAKNVPRQNSAPLL  
QTALLNGERPPGAKEAPPLTSLVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV  
RVASVQQVPPRLPPEARPGRRMFST SALQGAQGGARALLGGYSQAYGTVCHSALGHLPLL  
EGHHV

SEQ ID NO: 177\_N28606\_H, MOK\_H  
MKNYKAIGKIGEGTFSEVMKMQSLRDGNYYACKOMKQRFESIEQVNNLREIQALRRNLPH  
PNILMLHEVVFDKSGSLALICELMDMNIYELIRGRRYPLSEKKIMHYMYQLCKSLDHIH  
RNGIFHRDVKPENILIKQDVLKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLTDGFYT  
YKMDLWSAGCVFYEIASLQPLFGVNELDQISKIHDVIGTPAQKILTKFKQSRAMNFD  
FKKGSGIPLLTNLSPOCLSLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR  
KAGFPEHPVAPEPLNSCQISKEGRKQKQSLKQEE DRPKRRGPAYVMELPKLKLSGVVRL  
SSYSSPTLQSVLGS GTNGRVPVLRPLKCI PASKKTD PQDLKPAPQQCRLPTIVRKGG

SEQ ID NO: 178\_AB023153\_H, ICK\_H  
MNRYTTIRQLGDGTYSVLLGRSIESGELIAIKMKRKFYSWEECMNQREVKSLKKNLHA  
NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLPESAIRNIMYQILQGLAFIHLG  
FFHRDLKPENLLCMGP ELVKIADFLAREIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP  
IDVWAVGCIMAEVYTLRPLFGASEIDTIFKICQVLGTPKKT DWPEGYQLSSAMNFRWPQ  
CVPNNLKTLPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS  
EKPQKGILERAGPPPYIKPVPPAQPPAKPHTRISSRQHQASQPPLHLTPYKAEVSRTDH  
PSHLQEDKPSPLLP SLHNKHPQSKITAGLEHKNGEIKPKSRRRWGLISRSTKSDSDWAD  
LDDLDFSPSLSRIDLKNNKRSDDTL CRFESVLDLKPSEPVGTGNSAPTQTSYQRRDPT  
LRSAAQHLYLKHSRYLPGISIRNGILSNPGKEFIPNPWSSSGLSGKSSGTMSVISKVNS  
VGSSSTSSSGLTGNYVPSFLKKEIGSAMQVRHLAPI DPSPGYSSLKAMRPHPGRPFLDT  
QPRSTPGLIPRPPAAQPVHGRTDWASKYPSRR

SEQ ID NO: 179\_AA839940\_M  
SSNNGGMSAEEIIGPGAEPMRGPSLATRDWRDET VGT TDLQQGIDPGAVSPEPGKDHAHQ  
GPGRTEAGRVSSAAEAAIVLDDSAAPPFEHRVVS IKDTLISAGYTVSQHEVLGGGRF  
GQVHRCTERSTGLALAAKIIKVKNVKDREDVKNEVNIMNQLSHVNLIQLYDAFESKNSFT  
LIMEYVDGGELFDRI TDEKYHLTEL DVVLFTRQICEGVHYLHQHYILHLDLKPENILCVS

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## FIGURE 10

QTGHQIKIIDFGLARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL  
SGLSPFLGETDAETMNFIVNCSWDFDADTFKGLSEEAKDFVSRLLVKEKSCRMSATQCLK  
HEWLNHLPAKASGSNVRLRSQQLLOKYMAQSKWKHFHVVAAVNRLRKFTPCTP

SEQ ID NO: 180\_AA460132\_H  
MAAARATTPADGEEPAPAEALAAARERSRFLSGLELVKQGAEARVFRGRFQGRAAVIK  
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVFFVDYASNCLYMEEIEGSV  
TVRDYIQSTMETKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV  
LIDFGLSFI SALPEDKGVLDLYVLEKAFLLSTHPNTETVFEAFKSYSTSSKKARPVLKKLD  
EVRLRGRKRSMVG

SEQ ID NO: 181\_SGK034\_H  
QREKVNQGNMPLQSTFLAMDTEEGVEVVWNEHFGDRKAFAAHEEKIQTTFEQLVLVDH  
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKTKKNHKAMNARAWKRWCTQILS  
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALPDDLRSPIRAEREELR  
NLHFFPPEYGEVADGTAVDIFSGMCALEMAVLEIQTNGDTRVTEEAIAARARHSLSDPNM  
REFILCCLARDPARRPSAHSLLFHRVLFVHSLKLLAAHCFIQHQYLMPEENVVEEKTAM  
DLHAVLAELPRPRPPLQWRYSEVSFMELEDFVDRNGIYPLMNFAATRPLGLPRVLAP  
PPEEVQAKTPTPEPFDSETRKVIQMCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLL  
PTDSAQDLASELVHYGFLHEDDRMKLAFLSTFLKYRGTOA

SEQ ID NO: 182\_AA103218\_M SGK034\_M  
HASAPEYGEVNDGTGFVDIFSGMCALEMAVLEIQANGDTRVTEEAIAARARHSLSDPNMR  
EFILSCLARDPARRPSAHNLLFHRVLFVHSLKLLAAHCFIQHQYLMPEENVVEEKTAMD  
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLEDVDRNGIYPLMNFAAARPLGLPRVLAP  
PEEAQKAKTPTPEPFDSETRKVVQMCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLP  
TDSAQDLAAELVHYGFLHEDDRTKLAFLSTFLKYRGTOA

SEQ ID NO: 183\_NEK7\_H, N34132\_H  
MSGGAAEQSSTPGSLFLSPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT  
MDKDSRGAAATTTTEHRRFRSVICDSNATALELPGLPLSLPQPSIPAAVPQSAPPEPH  
REETVTATATSQVAQQPPAAAAPGEQAVAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPP  
ARSGSGGSAKEPQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVYKGLD  
TETVEVAWCELQDRKLTKEQRFKEEAEMKGLQHPNIVRFYDSWESTVKGKCCIVLV  
TELMTSGTLKTYLKRFKVMKIKVLRSWCRQILKGLQFLHTRTPLIHRDLKCDNIFITGP  
TGSVKIGDLGLATLKRASFASVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEY  
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIEGCIQONKDERYSIKDLLNHAFQ  
EETGVRVELAEDDGEKIAIKLWLRIEDIKKLKGYKDNEAIEFCFDLERDVPEDVAQEM  
VESGYVCEGDHKTMAKAIKDRVSLIKRKREQRQLVREEQENKKQEESLQQVEQSSASQ  
TGIKQLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQQLQYQQPSISVLSGDTVDSGQG  
SSVFTESRVSSQQTVSYGFPXHEQAHSTGTVPGHIPTVQAQSQPHGVYPPSSVQQGIQQ  
TAPPQQTQVQYSLSQTSSEATTAQPVSQPQAPQVLPQVSAGKQSTQGVSVQVAPAEVAV  
AQPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSRSRHE  
KTSRPKLRILNVSNKGRVVECQLETHNRKMVTFKFDLDGDNPEEIATIMVNDFILAIE  
RESFVDQVREIEKADEMLSEDVSVEPEGDQGLSLOGKDDYGFSGSQKLEGEFKQPIPA  
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN  
LSHSASSLSLQQAQFSELRAQMTEGPNTAPPNFSHTGPTFPVPPFLSSIAGVPTTAAAT  
APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVVTSGGLPIPPVSESPVLSSV  
SSITIPAVVISITTSPLSQVPTSTSEIVSSSTALYPSVTVSATSASAGGSTATPGPKPPA  
VVSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

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## FIGURE 1P

HSSTTGLAFSLAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL  
LPQVPSIPPLVQPVANVPAVQQTLIHSQPPALLPNQPHTHCPEVSDTQPKAPGIDDIK  
TLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP  
TNLPLGTVALPVTVPVTPGQVSTFVSTTTSGVKPGTAPSKPPLTKAPVLPVGTETLPGTL  
PSEQLPFPFGPSLTQSQQPLEDLDAQLRRTLSPEMITVTSVAVGPVSMAAPTAITEAGTQP  
QKGVSVQKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTESS  
VLSSSSPESTLVKPEPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKVGRFQVTTTAN  
KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVI PKKEKPELSEPSHLNGPSSD  
PEAAFLSRDVEDDGSQSPHSPHQLSSKSLPSQNLSSQSLNSFNSSSYMSSDNESDIEDDLK  
LELRLRLDKHLKEIQDLQSRQKHEIESLYTKLGKVP PAVI I PPAAPLSGRRRRPTKSKGS  
KSSRSSSLGNKSPQLSGNLSCQSAASVLHPQQT LHPGNI PESGQNQLLQPLKPSPSDN  
LYSAFTSDGAISVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184\_BCON3\_H  
MSEGESQTVLSSGSDPKVESSSAPGLTSVSPVSTTTSAASPEEEEESEDESEILEESP  
CGRWQKRREEVNQRNVPIDISAYLAMDTTEEGVEVVWNEVQF SERKNYKLQEEKVRVAFDN  
LIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLKKTCKNHKTMNEKAWKRW  
CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINN HVKTCREEQKNL  
HFFAPEYGEVTNVTAVDIYSFGMCALEMAVLEIQNGESSYVPQEAISSAIQLLEDPLQ  
REFIQKCLQSEPARRPTARELLFHPALFEVPSLKLAAHCIVGHQHMI PENALEEITKNM  
DTSVLAIEI PAGPGREPVTLYS QSPALELDFLEDVRNGIYPLTAFGLPRPQQQEEV  
TSPVPPSVKTPTEPEAEVETR KVVLMOQNI ESVEEGVKHHLTLLKLEDKLNRLSCDL  
MPNENI PELAAELVQLGFI SEADQSRLTSLLEETLNKFN FARNSTLNSAAVTSS

SEQ ID NO: 185\_AA711829\_M  
LKQFLKKTCKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK  
IGSVAPDTINN HVKTCREEQKNLHFFAPEYGEVTNVTAVDIYSFGMCALEMAVLEIQNG  
GESSYVPQEAISSAIQLLEDLSLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLAA  
AHCIVGHQHMI PENALEEITKNMDTSVLAIEI PAGPGREPVTLYS QSPALELDFLEDV  
RNGIYPLTAFGLPRPQQQEEVTSPVPPSVKTPTEPEAEVETR KVVLMOQNI ESVEEG  
VKHHLTLLKLEDKLNRLSCDLMPNESIPDLAAELVQLGFI SEADQSRLTSLLEETLNK  
FNFTRNSTLNTATVTSS

SEQ ID NO: 186\_AA099102\_H  
MSSCVSSQSSNRAAPQDELGGRGSSSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP  
GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR  
CICPSLPYSPVSSPQSSPRLPRRPTVESHHV SITGMQDCVQLNQYTLKDEIGKGSYG VVK  
LAYNENDNTYYAMKVL SKKKLIRQAAPRRPPRGRTRPAPGGCIQPRGPIEQVYQEIAIL  
KKLDHPNVVKLVEVLDDPNEDHLYMV FELVNQGPVMEVPTLKLSEDQARFYFDLI KGI  
EYLHYQKI IHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGT PAFMAPESLS  
ETRKFISGKADVWAMGVTL YCFVFGQCPFMDERIMCLHSKIKSQALEFPDQPDIAEDLK  
DLITRMLDKNPESRIVVPEIKLHPWVTRHGAEP LPSDENCTLVEVTEEEVENS VKHIP  
LATVILVKT MIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP  
PGRHPAPRGGGSALVRGSPCVESCWAPAPGSPARMHPLRPEEAMEPE

SEQ ID NO: 187\_5R69\_17\_2\_H  
MQEIPQEQIKEIKKEQLSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVR  
QTFNKEIKTMKKFESPNILRIFGICIDETVTPPQFSIVMEYCELGT LRELLDREKDLTLG

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## FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSMSLGTT  
REKTDREVSTAYLSPQELEDFYQYDVKSEIYSFGIVLWEIATGDI PFQGEEDWLSQW  
L

SEQ ID NO: 188\_H85811\_H

MAPVYEGMASHVQVFSPTLQSSAFCSVKKLKIEPSSNWDMTGYGSHSKVYSQSKNIPLS  
QPATTTVSTSLPVPNPSPYEQTI VFPGSTGHIVVTSASSTSVTGQVLGGPHNLMRRSTV  
SLLDYQKCGCLKRKSEEIENTSSVQIIEEHPPMIQNNASGATVATATTSTATSKNSGSNS  
EGDYQLVQHEVLCMTNTYEVLEFLGRGTGQVVKCWKRGTEI VAIKILKNHPSYARQG  
QIEVSILARLSTESADDYNFVRAYECFQHKNTCLVFEMLEQNLDFLKQNKFSPLPLKY  
IRPVLLQVATAMKLSGLIHADLKPENIMLVDPSPRPYRVKVIDFGSASHVSKAVCST  
YLSRYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPGDSEYDQIRYISQTQGLP  
AEYLLSAGTKTTRFFNRDTSPLYLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVN  
MTTDLGSDMLVEKADRRFIDLLKMLTIDADKRITPIETLNHPFVTMTHLLDFPHSTH  
VKSCFQNMIECKRRVNMVDTVNQSKTPFI THVAPSTSTNLMTFNNQLTTVHNQPSAASM  
AAVAQRSMPLQTGTAQICARPDFFQQAALIVCPGFGQLQASPSKHAGYSVRMENAVPIVT  
QAPGAQPLQIQPGLLAQQA WPSGTQQIILLPPAWQQLTG VATHTSVQHATVIPETMAGTQQ  
LADWRNTHAHGSHYNPIMQQPALLTGHVTLPAAPLNVGVAHVMRQQPTSTSSRKSKQH  
QSSVRNVSTCEVSSSQAISSPQSRKRVKENTPPRCAMVHSSPACSTSVTCGWGDVASSTT  
RERQRQTIVIPDTPSPVSVITISSDTDEEEEQKHAPTSTVSKQRKNVISCVTVHDSPLS  
DSSNTSPYSVQQRAGHNNANAFDTKGSLENHCTGNPRTIIVPPLKTQASEVLVECDLSL  
PVNTSHHSSSYKSSSNVTSTSGHSSGSSSGAITRQQRPGPHFQQQQPLNLSQAQQHI  
TTDRGTGSHRRQAYITPTMAQAPYSFPHNSPSHGTVHPLAAAAAAHLPTQPHLYTYTA  
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQPVPVSMGPRVLPSTIHP SQYPAQF  
AHQTYISASPASTVYTGYP LSPAKVNQYPYI

SEQ ID NO: 189\_DYRK3\_H

MMIDETKCPPCSNVLCNPSEPPPPRRRLNMTAEQFTGDHTQHFLDGGEMKVEQLFQEFGNR  
KSNTIQSDGISDSEKCSPTVSQKSSDCLNTVKSNSSSKAPKVPLTPEQALKQYKHHLT  
AYEKL E I INYPEIYFVGPNAKKRHGVIGGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII  
GKGSFGQVARVYDHKL RQYVALKMVRNEKRFHRQAAEEIRILEHLKKQDKTGSMNVIHML  
ESFTFRNHVCMFELLSIDLYELIKKNKFQGF SVQLVRKFAQSILQSLDALHKNKIIHCD  
LKPENILLKHHGRSSTKVIDFGSSCFEYQKLYTIQSRFYRAPEIILGSRYSTPIDIWSF  
RCILAE LLTGQPLFPGEDEGDQLACMELLGMPPPKLLEQSKRAKYFINSKGI PRYCSVT  
TQADGRVVLVGGRSRRGKRGPPGSKDWGTALKGCDDYLFIEFLKRC LHWDP SARLTPAQ  
ALRHPWISKSVPRPLTTIDKVSGKRVVNPASAFQGLGSKLPPVVGIANKLKANLMSETNG  
SIP LCSVLPKLIS

SEQ ID NO: 190\_AA589241\_M DYRK3\_M

TRPELLGMPPQKLLLEQSKRAKYFINSKGLPRYCSVSTQTDGRVVLLGGRSRRGKRGPPG  
SKDWATALKGCGDYLFIEFLKRC LQWDPSARLTPAQALRHPWISKSTPKPLTMDKVPGKR  
VVNPTNAFQGLGSKLPPVVGIA SKLKANLMSETSGSIP LCSVLPKLIS

SEQ ID NO: 191\_5R72\_16\_2\_H

MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACGPVKEPPEINLVLY  
PQGLTGEEVYVKVDLRVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLLELAKKHCGE  
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQORLLEAKRKEEQEQRILHEIQ  
RRKEEIKEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAI LHGGSPDFVGNKGHR  
ANSSGRSRRERQYSVCNSEDSPGSC EILYFNMGSPDQLMVHKGKIGSDEQLGKL VYNAL  
ETATGGFVLLYEWVLQWQKMGPF LT SQEKEKIDKCKKQIQGTETEFNSLVKLSHPNVVR

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## FIGURE 1R

YLAMNLKEQDDSIIVDILVEHISGVSLAAHLSHSGPIPVHQLRRYTAQLLSGLDYLSNS  
 VVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGD  
 VWRLGLLLLLSLQSQECGEYPTIPSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFIN  
 PQPKMPLVEQSPEDSGGQDYVETVIPS NRLPSAAFFSETQRQFSRYFIEFEELQLLGKGA  
 FGAVIKVQNKLDGCCYAVKRIPIPNASRQFRRIKGEVTLLSRLHHENIVRYNAWIERHE  
 RPAGPGTPPPDSGPLAKDDRAARGQPASDTDGLDSVEAAAPPPILSSSVEWSTSGERSAS  
 ARFPATGPGSSDDEDDDEHGGVFSQSFLPASDSEDIIFDNEDENS KSNQDEDCNEK  
 NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH  
 EKGMIHRDLKPVNIFLSDDDHVKIGDFGLATDHLAFSADSKQDDQTDGLIKSDPSGHLTG  
 MVGTALYVSPEVQGSTKSAYNQKVDLFLSGIIFFEMSYHPMVTASERIFVLNQLRDPSTP  
 KFPEDFDDGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPPQMEESSELHEVLHHTLT  
 NVDGKAYRTMMAQIFSQRISPAIDYTYDSILKGNFSIRTAKMQQHVCETIIRIFKRHGA  
 VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIE  
 RVFRPRKLDRFHPKELLECAFDIVTSTTNSFLPTAEIITYIYEIIQEFPAQERNYSIYL  
 NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSLSNSLCRLYKF  
 IEQKGLDQDLMPNTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYK  
 VQQHNGIIFQFVAFIKRRQRAVPEILAAGGRYDILLIPQFRGPQALGPVPTAIGVSIADK  
 ISAAVLNMEESVTISSCDLLVSVGQMSMRINLTQKLWTAGITAEIMYDWSQSQEELQ  
 EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETTELVDHVLQKLRTKVTDERNG  
 REASDNLAVQNLKGSFNSASGLFEIHGATVVPVIVSVLAPEKLSASTRRRYETQVQTRLQT  
 SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC  
 DEIYNIKVEKKVSVLFLYSYRDDYYRILF

SEQ ID NO: 192\_R43524\_H, HRI\_H  
 MLGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQOQTFP  
 FAVANQLLLVSLLEHLSHVHEPNPLRSRQVFKLLCQTFIKMGLLSFTCSDEFSSRLHH  
 NRAITHLMRSKERVQRDPCEDISRIQKIRSREVALEAQTSTRYLNEFEELVILGKGGYGR  
 VYKVRNKLDGQYYAIKKILIKGATKTVCMKVLREVKVLAGLQHPNIVGYHTAWIEHVHI  
 QPRADRAAIELPSLEVLSDQEEDREQCGVKNDSSSSSIIFAEPTPEKEKRFGESDTENQ  
 NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQLPLRRNSHLEESFTSTEE  
 SSEENVNFLGQTEAQYHMLHIQMQLCELSLWDWIVERNKRGREYVDESACPYVMANVAT  
 KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTNRN  
 GKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSLGVVLELFQFPFGTEMERAEVLTGL  
 RTGQLPESLRKRCVPQAKYIQHLTRRNSSQRPSAIQLLQSELFQNSGNVNLTLMKII EQ  
 EKEIAELKKQLNLLSQDKGVRDDGKDGCVG

SEQ ID NO: 193\_17000057519457\_H  
 MAAARATTPADGEEPAPAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK  
 HRFPGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVFFVDYASNCLYMEETEGSV  
 TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV  
 LIDFGLSFISALPEDKGVLDYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD  
 EVRLRGRKRSMVG

SEQ ID NO: 194\_AA013524\_M  
 LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPELEARLGRRRTVQEARALLRCRRAGIA  
 APVFFVDYASNCLYMEETIEDSVTVRDYIQSTMETEKDPQCLLDLARRMGQVLGMHDQD  
 LIHGDLTTSNMLLRPLAQLHIVLIDFGLSFVSGLPEDKGVLDYVLEKAFLSTHPHTETA  
 FEAFLKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

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## FIGURE 1S

SEQ ID NO: 195\_17000139801197\_H, IRAKM\_H  
MAGNCGARGALSAHTLLFDLPPALLGELCAVLDS CDGALGWRGLAERLSSSWLDVRHIEK  
YVDQKSGTRELWLSWAQNKKTIGDLLQVLQEMGHRRAIHLITNYGAVLSPSEKSYQEGG  
FPNILFKETANVTVDNVLIPHENEKGVLLKSSISFQNTIEGTRNFHKDFLIGEGEIFEVY  
RVEIQNLTYAVKLFKQEKMKQCKKHWRFLSELEVLFFFHHPNILELAAYFTETEKFCCLI  
YPYMRNGTLFDRLOQCVGDTAPLPWHIRIGILIGISKAIHYLHNVPQCSVICGSISSANIL  
LDDQFQPKLTDFAHAFRSHLEHQSTINMTSSSSSKHLWYMPEEYIRQKLSIKTDVYSF  
GIVIMEVLTGCRVVLDDPKHIQLRDLRELMEKRGDLSCLSFDDKKVPPCPRNFSAKLFC  
LAGRCAATRAKL RPSMDEVLTLESTQASLYFAEDPPTSLKSFRCPSPLFLENVPSIPVE  
DDESQNNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPESKRNEEACNMPSSSSCE  
ESWFPKYIVPSQDLRYPKVNIDPSSEAPGHSCSRPVESSCSSKFSWDEYEYQYKKE

SEQ ID NO: 196\_AA840598\_M IRAKM\_M  
MWKRFLSELEVLFFFHHPNILELAAYFTETEKLCVYPYMSNGTLFDRLOQCTNGTTPLSW  
HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANILLDDQLQPKLTDFAAAHFRPNLEQQ  
SSTINMTGGGRKHLWYMPEEYIRQGRSLVKTDVYSFGIVIMEVLTGCKVVLDDPKHVQLR  
DLLMELMEKRGDLSCLSFDRKIPPCPRNFSAKLFSLAGRCVATKAKLRPTMDEVLSLE  
STQPSLYFAEDPPTSLKSFRCPSPLFLDNVPSIPVEDDENQNNHSPVPPKEVLGTDRVTQK  
TPFECSQSEVTLFLGLDRNRGNRGSEADCNVSSSHEECWSPELVAPSQDLSPTVISLGSS  
WEVPGHSYGSKPMKRCSSGLFCSEHEQSKKO

SEQ ID NO: 197\_AA088547\_H  
MASAVRGSRPWPRLGLQLQFAALLLGTLSPQVHTLRPENLLLSTLDGSLHALSKQTGDL  
KWTLRDDPVIIEGPMYVTEMAFLSDPADGSLYILGTQKQQLMKLPFTIPELVHASPCRSS  
DGVFYTGKQDAWFVVDPESETQMTLTTEGPSTPRLYIGRTQYTVTMHDPAPALRWNT  
TYRRYSAPPMDGSPGKYMHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTWHDGL  
RQLPHLTLDLTLHFLALRWGHIRLPASGPRDTATLFTLDTQLMTLYVGKDETGFYVS  
KALVHTGVALVPRGLTLAPADGPTTDEVTLPQVSGEREGSPSTAVRYPSGSVALPSQWLLI  
GHHELPPVLHTTMLRVHPTLGSGTAETRPENTQAPAFFLELLSLSREKLWDSELHPEEK  
TPDSYLGLGPQDLLAASLTAVLLGGWILFVMRQVVEKQOETPLAPADFAHISQDAQSLHS  
GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGTFFVRGQFEGRA  
VAVKRLRECFGLVRREVQLLQESDRHPNVLRYFCTERGPOFHYIALELCRASLQEYVEN  
PDLDRGGLEPEVVLQQLMSGLAHLHSLHIVHRDLKPGNIIITGPDSSQLGRVVLSDFGLC  
KKLPAGRCFSLSHSGIPGTEGWMAPELLQLLPDPSPTSAVDIFSAGCVFYVLSGGSHPF  
GDSLYRQANILTGAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAHPFFWSR  
AKQLQFFQDVSVDWLEKESEQEPLVRALEAGGCAVVRDNWHEHISMPLOTDLRKFRSYKGT  
SVRDLLRAVRNKKHHYRELPEVVRQALGQVPDGFVQYFTNRFPRLLLHTRAMRSCASES  
LFLPYYPDPSEARRPCPGATGR

SEQ ID NO: 198\_HGP\_6644466  
MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRSRGLSHSP  
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGGE  
KSLNDLIEERYKASQDPFPAIILKVALNMARGLYLHQEKLLHGDIKSSNVVIKGDFF  
TIKICDVGVSPLDENMTVDPEACYIGTEPWPKPEAVEENGVIDKADIFAFGLTLWEM  
MTLSIPHINLSNDDDDDEKTFDESDFDDEAYYAALGTRPPINMEELDESQKVIELFSVC  
TNEDPKDRPSAAHIVEALETDV

SEQ ID NO: 199\_AA449542\_M  
SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKSLHHPNIVGYRAFTEASDGL  
CLAMEYGGESLNDLIEERNKDSGSPFAAVILRVALHMARGLYLHQEKLLHGDIKSS

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## FIGURE 1T

NVVIKGFETIKIKCDVGVSLPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADV  
AFGLTLWEMMTLCIPHVNLPDDDDVEDATFDESDFDEAYYAALGTRPSINMELDDSYQK  
AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200\_5R57\_10\_2\_M TESK2\_M  
LLDSDLYLPWTVRVKLAYGIAVGLSYLHFKGIFHRDLTSKV

SEQ ID NO: 201\_AA232253\_H  
MSSLGASFVQIKFDDLQFFENC GGSGSVYRAKWISQDKEVAVKLLKIEKEAEILSVL  
SHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMHIMTWATDVAKGMHY  
LHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMSLVGTFPWWAPEV IQS  
LPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQVAWLVEKNERLTIPSSCPRSFAELLH  
QCWEADAKKRPSFKQIIISILEMSNDTSLPDKNSFLHNKAWEKCEIEATLERLKKLERD  
LSFKEQELKERERRLKMWEQKLTEQSNTPLLPSFEIGAWTEDDVYCWVQQLVRKGDSSAE  
MSVYASLFKENNITGKRLLLLEEDLDKMGIVSKGHIHFKSAIEKLTHDYINLFHFPPL  
IKDSGGEPEENEKIVNLELVFGFHLKPGTGPDCKWKMYMEMDGEIAITYIKDVTFTNT  
NLPDAEILKMTKPPFVMEKWIIVGIAKSQTVECTVTYESDVRTPKSTKHVHLIQWSRTKPQ  
DEVKAVQLAIQTLFTNSDGNPGRSDSSADQWLDTLRMRQIASNTSLQRSQSNPILGSP  
FFSHFDGQDSYAAAVRRPQVPIKYQOITPVNQSRSSSPTQYGLTKNFSSHLNSRDSGFS  
SGNTDTSSERGRYSDRSRNKYGRGSIISLSSPRGRYSGKSQHSSTPSRGRYPGKFYRVSQS  
ALNPHQSPDFKRSRDLHQPNTPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP  
SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202\_AI375137\_H  
MGNYKSRPTQTCTDEWKKKVSESYVITIERLEDDLQIKEKELTELNRNIFGSDEAFSKVNL  
NYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL  
LHSGADIQQVGYGGLTALHIATAGHLEAADVLLQHGANVNIQDAVFFTPLHIAAAYYGHE  
QVTRLLLKFADVNVSSEVGDRLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVLH  
FCSRFGHHDIVKYLQSDLEVQPHVNIYGDTPHLHLACYNGKFEVAKIEIIQISGTESLTK  
ENIFSETAFHSACTYGKSIDLVKFLLDQNVININHQRDGTGLHSACYHGHIRLVQFLL  
DNGADMNLVACDPSRSSGEKDEQTCMLWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG  
GDGSYVSVSPPLGKIKSMTKEKADILLRAGLPSHFHLQLSEIEFHEIISGSGFGKVYKG  
RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCVIQFVGACLNDPQSQAIVTQ  
YISGGSLSLLEHQKRILDLQSKLIIAVDVAKGMEYLHNLTQPIIHRDLNSHNILLYEDG  
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT  
GEIPFAHLKPAAAAAD MAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE  
ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA  
LSQSAGQYSSQGLSLEEMKRSLQYTPIDKYGYVSDPMSSMHFHSRNSSSFEDSS

SEQ ID NO: 203\_H97685\_H  
MESERSPLYRQLIDLGYLSSSHWNCGAPGQDTKAQSMLEQSEKLRHLSTFSHQVLQTRL  
VDAAKALNLVHCHCLDIFINQAFDMQORDLQITPKRLEYTRKKENELYESLMNIANRKQEE  
MKMDIVETLNTMKEELLDDATNMEFKDVI VPENGEVGTREIKCCIRQIQELIISRLNQA  
VANKLISSVDYLRESFVGTLERCLQSLEKSQDVSVHITSNYLKQILNAAHYHEVTFHSGS  
SVTRMLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAKSICSQFRTRLNS  
SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHPRLARLSLESRLQDVLLHRKPKLG  
QELGRGQYGVVYLCDNWGGHFPALKSVVPDEKHWNDLALEFHYMRSLPKHERLVDLHG  
SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH  
RDIKLNVLDDKQNRKITDLGFCCKPEAMMSGSI VGTPIHMAPELFTGKYDNSVDVYAFG

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## FIGURE 1U

ILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDGDPLK  
RPLLGIQVQMLQGIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204\_W20810\_M

DVNLKASKASDVYSFGILVWAVLAGREAELVDKTSI RETVCDRQSRPPLTELPPGSPET  
PGLEKLKELMIHCWGSQSENRP SFQDCEPKTNEVYNLVKDKVDAAVSEVKHYLSQHRSSG  
RNLSAREPSQRGTMDCPRET MVSKMLDRLHLEEPSGPVPGKCPERQAQDTSVGPATPAR  
TSSDPVAGTPQIPHTLPFRGTTGPGVFTETPGPHQORNQGDGRHGTWPYPWTPPNPMTGP  
PALVFNNCSEVQIGNYNLSLVAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205\_AA744236\_H

MGSENSALKSYTLREPPFTLPSGLAVYP AVLQDGKFASVFVYKRENEDKVNKA AKHLKTL  
RHPCLLRFLSCTVEADGIHLVTERVQPLEVALETLSAEVCAGIYDILLALIFLHDRGHL  
THNNVCLSSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRD PASIPPEEMSPEFTT  
LPECHGHARDAFSFGTLVESLLTILNEQVSADVLSSFQOTLHSTLLNPIPKCRPALCTLL  
SHDFFRND FLEVVNFLKSLTLKSEEEKTEFFKFLLD RVSC LSEELIASRLVPLLNLQLVF  
AEPVAVKSF LPYLLGPKKDHAQGETPCLLS PALFQSRVIPVLLQLFEVHEEHVRMVLISH  
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGERTKI  
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSDVKNTSEDS ENFPSSSKSEWPDWSE  
PEEPENQTVNIQIWPREP CDDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV  
TSGEQKPIPALLSLTEESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSELG  
LGEEFTIQVKKKPVKDPMDW FADMIPEIKPSAAFLILPELRT EMVPKKDDVSPVMQFSS  
KFAAAEITEGEAEGWEEEGELNWNEDNNW

SEQ ID NO: 206\_AI052250\_H

MESMLNKLKSTVTKVTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE  
VAVFVFDKKLIDKYQKFEKDQIIDSLKRGVQQLTRLRHPRLTLVQHPLEESRDCLAFCTE  
PVFASLANVLGNWENLPSPISPDIKDYKLYDVETKYGLLQVSEGLSFLHSSVKMVHGNIT  
PENIILNKSGAWKIMGFD FCVSSTNPSEQEPKFPCKEWDPNLP SLCLPNPEYLAPEYILS  
VSCETASDMYSLGTVMYAVFNKGKPIFEVNKQDIYKFSRQLDQLSRLGSSSLTNIPEEV  
REHVKLLLNVTPTVRPDADQMTKIPFFDDVGAVTLQYFDTL FQRDNLQKSQFFKGLPKVL  
PKLPKRIVIVQRIPLCTSEFVNPDMPVFPVLPNVLLIAEECTKEEYVKLILPELGPVFKQQ  
EPIQILLIFLQKMDLLLT KTPPDEIKNSVLPMVYRALEAPSIQIQELCLNI IPTFANLID  
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207\_AA278842\_H

MWFFARDPVRDFPFELIPEPPEGGLPGPWALHRGRKKATGSPVSI FVYDVKPGAEEQTQV  
AKAAFKRFTLRHPNILAYIDGLETEKCLHVTEAVTPLGIYLKARVEAGGLKELEISWG  
LHQIVKALSFLVNDCSLIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQNGGGGPPRKGIPE  
LEQYDPP ELADSSGRVREKWSADMWRLGCLIWEVFNGPLPRAAALRNPGKIPKTLVPHY  
CELVGANPKVRPNPARFLQNCRAPGGFMSNRFVETNLFLEEIQIKEPAEKQKFFQELSKS  
LDAFPEDFCRHKVLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVKMFSS  
TDRAMRIRLLQMEQFIQYLDEPTVNTQIFPHVVHGFLDTNPAIREQTVKSMLLLAPKLN  
EANLNVELMKHFARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPF  
APSRVAGVLGFAATHNLYSMNDCAQKILPVL CGLTVDPKSVRDQAFKAIRSFLSKLESV  
SEDPTQLEEVEKDVHAASSPGMGGAASWAGWAVTGVS SLT SKLIRSHPTTAPTETNIPQ  
RPTPEGVPAPAPTVPATPTTSGHWETQEEDKDTAEDSSTADRWDEDWGSLEQEAESVL  
AQDDWSTGGQVSRASQVNSDHKSSKSPESDWSSWEAEGSWEQGWQEPSSQEP PPDGTR  
LASEYNWGGPESSDKGDPFATLSARPSTQPRPDSWGEDNWEGLETDSRQVKAELARKRE  
ERRREMEAKRAERKVAKGPMKLGARKLD

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## FIGURE IV

SEQ ID NO: 208\_AA599286\_H  
MAFMEKPPAGKVLLDDTVPLTAAIEASQSLQSHTEYIIRVQGGISVENSWQIVRRYSDFD  
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD  
PNNYSANYTEIALQQVSMFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLWS  
ADLGPDKYLSKDFQCLIKLLPSCLHPYIYRVTFATANESSALLIRMFNEKGTLDLIYK  
AKPKDPFLKKYCNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFPYGHLLHASNVMLDGD  
CRLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP  
PAPSMVAVVLESTLSCEACKNGMPTISRLLQMPFLSDVLLTSEKPFKIPTKLKEALR  
IAKECIEKRLIEEQKQIHQHRRLTRAQSHHGSEERKKRILARKKSKRSALENSEEHS  
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEAPAQLS  
SQAVNGMSRGALLSSIQNFQKGTLRKAKPVITVLRSSAEASCLHLEGKVLFSYSPLPPN  
YPLPGKVIAPVQPPQTVLFCRCSCQKLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209\_AA425725\_H  
MSASTGGGGDSGGSSSSSQASCGPESSGSELALATPVPQMLQGLLGSDDDEEQEDPKD  
YCKGGYHPVKIGDVFNGRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVVKSAHYTETA  
VDEIKLLKCVRDSDPSDPKRETIQVLIIDDFRISGVNGVHVCMLVLEVLGHQLLKWIIKSNY  
QGLPVPCVKSIVRQVLHGLDYLHTCKCKIHTDIKPENILLCVGDAYIRRLAAEATEWQQA  
GAPPPSRISIVSTAPQEVLTGKLSKNKRKKMRKRKQKRLLEERLRLDLQRLAMEAATQA  
EDSGRLDGGSGSTSSSGFSGSLFSPASCSILSGSSNQRETGGLLSPSTPFGASNLLVNP  
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEGPPADIWSTACMAF  
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDIPPAFALSGRYSREFFNRRGELRHIHN  
LKHGGLYEVLMEKEYEWPLEQATQFSAFLLPMMEYIPEKRASAADCLQHPWLN

SEQ ID NO: 210\_SGK022\_H  
MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ  
IVRTL DHKNI IQVYEMLESADGKICLVMELEAGGDVFDVNLGGPLPESRAKALFROMVE  
AIRYCHGCGVAHRDLKCNALLQGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEV  
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSPFTHLSISADCQD  
LLKRLLPEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 211\_AA060026\_M\_SGK022\_M  
MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFIQRFLPRELQ  
IVRTL DHKNI IQVYEMLESADGKIYLVMELEAGGDVFDVNLGGPLPESRAKALFROMVE  
AIRYCHGCGVAHRDLKCNALLQGFNLKLTDFGFAKVLPKSRRELSQTFCGSTAYAAPEV  
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSPFTHLGISTECQD  
LLKRLLPEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 212\_AA399669\_H  
MGKGDVLEAAPTTTTAYHSLMDEYGYEVGKAIGHGSYGSVYEFYTKQKVMVAVKIISSKK  
ASDDYLNKFLPREIQQVMKVL RHKYLINFYRAIESTSRVYIIILEAQGGDVLEWIQRYGA  
CSEPLAGKWFSQTLGIAYLHKSIVHRDLKLENLLLDKWENVKISDFGFAKMVPSPNQPV  
GCSPXYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVVVAHLPF  
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213\_AA758539\_H  
MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE  
MDILATVNHGSIKTYEIFETSDGRIYIIMELGVQGDLLLEFIKCGALHEDVARKMFRQL  
SSAVKYCHDLDIVHRDLKCNLLLDKDFNIIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

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FIGURE 1W

YAAPEVLQSIPIYQPKVYDIWSLGVILYIMVCGSMFYDDSDIRKMLRIQKEHRVDFPRSKN  
LTCECKDLIYRMLQPDVSQLHIDEILSHSWLQPPKPKATSSASFKEGEGKYRAECKLD  
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMDRLAETSRADHHSISGAEVGKAST

SEQ ID NO: 214\_AA883975\_H  
MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKYKGTVAIKVVDRRRAPPDFVNKFLPRE  
LSILRGVVRHPHIVHVFIEVFCNGKLYIVMEAAATDLLQAVQNRGRI PGVQARDLFAQIA  
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGRAHQAGYPDLSTTYCGSAAAYASP  
EVLLGIPYDPKPYDVWSMGVVLVMTGCMFDDSDIAGLPRRQKRGVLYPEGLELSERC  
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215\_AA905446\_H  
VGRQETGVRRWAFLICQIPSPPLTSSEFIQRFPLPRELQIVRTL DHKNI IQVYEMLESADG  
KICLVMELAEAGDVFDCVLNGGGLPESRAKALFROMVEAIRYCHGCGVAHRDLKCENALL  
QGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEVLQGI PXKMLWQQQKGVSFPTH  
SISADCQDLLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 216\_H29974\_H  
YSLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV  
VQFEECVLQRNGLAQRM SHGNKSSQLYLRLVETSLKGERILGYAEPCYLWFMFCEGG  
DLNQYVLSRRPD PATNKSFMLQLTSAIAFLHKNHIVHRDLKPDNILITERSGTPILKVAD  
FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYMAPEVWEGHYTAKADIFALG  
IIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLENPKMELHIPQKRRTSMSEG  
IKQLLKDMLAANPQDRPDAFELETRMDQVTCAA

SEQ ID NO: 217\_AA498104\_M H29974\_M  
PLLLPPPPAAMETGKENGARRGKSPERKRRSPVQORVLC EKL RPAAQAMPAGAEVPGEA  
FLARRRPDGGGDV PARPRYSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVE  
LALAEFWALTSLKRRHQNVVQFEECVLQRNGLAQRM SHGNKNSQLYLRLVETSLKGERIL  
GYAEPCYLWFMFMEYCEGGDLNQYVLSRRPD PATNKSFMLQLTSAIAFLHKNHIVHRDLK  
PDNILITERSGTPILKVAD FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYM  
APEVWEGHYTAKADIFALGIIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLE  
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPDAFELETRMDQVTCAA

SEQ ID NO: 218\_AA215311\_H  
MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI  
KSQHPNVIHLEECILQKDMVQKMSHGSNSSLYLQLVETSLKGEIAFDPR SAYYLWFMVD  
FCDGGDMNEYLLSRKPNRKTNTSFMLQLSSALAF LHKNI IHRDLKPDNILISQTRLDTS  
DLEPTLKVADFGLSKVCSASGQNPEEPVSVNKCFLSTACGTFYMAPEVWEGHYTAKADI  
FALGIIIWAMLERITFIDTETKKELLGSYVKQGT EIVPVGEALLENPKMELLI PVKKKSM  
NGRMKQLIKEMLAANPQDRPDAFELELRLVQIAFKDSSWET

SEQ ID NO: 219\_AA018361\_H  
MRAAFPAGGAGGSVEPPSARPAPQAGTAARSEEAPARAQAAGMAGPGWGPRLDGFILT  
ERLGS GTYATVYKAYAKKDTREVVAIKCVAKKSLNKASVENLLTEIETLKGIRHPHIVQL  
KDFQWSDNIYLI MEFCAGGDL SRFIHTRILPEKVARVFMQQLASALQFLHERNISHLD  
LKPQNILLSSLEKPHLKLADFGFAQHMSPWDEKHLVLRGSPLYMAPEMVQORQYDARVDLW  
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDLLQRLLERDPSR  
RISFQDFFAHPWVDLEHMPSGESLGRATALVVQAVKKDQEGDSAAALS LYCKALDFFVPA

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## FIGURE 1X

LHYEVDAQRKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARKPRLL  
 AALEVASAAMAKEEAAGGEQDALDLYQHS LGELL LLLRS PRAGGSCFTLRFR TSWPELN  
 T

SEQ ID NO: 220\_AA311714\_H  
 MENFILIYEEIGRGSKT VVYKGRRKGTIN FVAILCTDKCRRPEITNWVRLTREIKHKNIVT  
 FHEWYETSNHLWLXENLPEDVVREFGIDLISGLHHLHKLGLFCDISPRKILLEGPGTL  
 KFSNFCLAKVEGENLEEFFALVAAEEGGGDNGENVLKKSMKSRVKGSPVYTAPEVVRGAD  
 FSISDLWSLGLLYEMFSGKPPFFSESVSELTEKILCEDPLPPIPKDSSRPKASSDFIN  
 LLDGLLQRDPQKRLTWTRLLQHSFWKKA FAGADQESSVEDLSLSRNTMECSGPQDSKELL  
 QNSQSRQAKGHKSGQPLGHSFRLENPTFRPKSTLEGQLNESMFLSSRPTPTSTAVEV  
 SPGEDMTHCSPOKTSPLTKITSGHLSQQDLESQMRELIYTDSDLVVTPIIDNPKIMKQPP  
 VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV  
 AGHQEVATRLLHSPFLQLLIQHLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS  
 SIGIGILNCLVQHSTPVPRQCLVYV

SEQ ID NO: 221\_SGK384\_H  
 SLAHVLRARQILTEPEVRDYLRLGLVSGLRYLHQRCILHR

SEQ ID NO: 222\_AA210451\_M SGK384\_M  
 MGQQHGTRNGLTHRELPRGVGLLLAMALMNVALYLCLDQLFISPRSTADSRRCPPGYFR  
 MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH  
 GLQMLKSLQSEHVVTLVGYCEEDGTILTEYHPLGSLSNLEETLNL SKYQDVNTWQHRLQL  
 AMEYVSIINYLHHSPLGTRVMCDSDNLPKTL SQYLLTSNFSI VANDLDALPLVDHDSGV  
 IKCGHRELHGDFVAPEQLWPYGEDTPFQDDLMPSYNEKVDIWKIPDVSSFLLGHVEGSDM  
 VRFHLFDIHKACKSQIPAERPTAQNVLDAYQRVFHSRLRDTVMSQTKEML

SEQ ID NO: 223\_SGK071\_2\_H  
 EVVAVQMMVECMDDHYASQALEELMPLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF  
 NELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDAL EYLHHLDI IHRNLKPSNIILISSDH  
 CKLQDLSSNVLMTDKAKWNIRAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIIIDMTSC  
 SFMDGTEAMHLRKSRLRQSPGSLKAVLKTMEEKQIPDVETFRNLLPLMLQIDPSDRITIKD  
 VVHITFLRGSFKSSCVSLTLHRQMPASITDMLLEGNVASILGDAGDTKGERALKLLSMA  
 LASYCLVPEGS LFMPLALLHMDQWLSCDQDRVPGKRD FASLGKLGKLLGPIPKGLPWPP  
 ELVEVVVTTMELHDRVLDVQLCACSLLLHLLGQALVHHPEAKAPCNQAITSTLLSALQSH  
 PEEEP LLVMVYSLLAITTTQESSELS EELQNA GLL EHLNSSLERSDVCASGLGLLW  
 ALLLDDPILALQRP RKRAPNHGKPGKPNPASTQSIIVNKAPLEKVPDLISQVLATYPA  
 DGEMAEASCGVFWLLSLLGCIKEQQFEQVVALLLQSIRLCQDRALLVNNAYRGLASLVKV  
 SELAAFKVVVQEEGGSGLSLIKETYQLHRDDPEVVENVGM LLVHLASYEEILPELVSSSM  
 KALLQEIKERFTSSSLVSDSSAFSKPGLPPGSPQLGCTTSGGLE

SEQ ID NO: 224\_AA118352\_M SGK071\_M  
 EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIIIDMATCSFLNDTEAMQLRKAIRHHPGSL  
 KPILKTMEEKQIPGTDVYYLLLPFMLHINPSDLRAIKDVMQVT FMSNSFKSSVALNMQR  
 QKVPIFITDVLLLEGNMANILGSWLCASFVND SRHCD SGIGSQR LGFD FQSVSWTEHPLKD  
 VMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTELLEVISI IKQHGRILDILLSTCSLL  
 LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSQGI SEEL  
 EEEGLFQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP  
 EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVLLLLRSIQLCPGRVLLVNNAFRGLASLAK

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## FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG  
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGQLQEDQLEPPAGQEAPLQGEPLFRP

SEQ ID NO: 225\_018653.9\_H

GRGRGAGHARGLRGPAGRAEPPRSLSRPGPGPSRAGPAGRGEESDAAPAGGSGRGFL  
RLLPAGLRPQALRSGSEPPRPGQSPEPSPAPGAGRRGGRGELARQIRARYEEVQRYSRG  
GPGPGAGRPERRRLMDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA  
ALRNVSGAQYMGSGYTKAVYRVRLPGGAVALKAVDGSGHDLGSCVREFGVRRGCYRLAA  
HKLLKEMVLLERLRHPNVLQLYGYCYQDSEIPDTLTTITELGAPVEMIQLLQTSWEDRF  
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI  
LEFPARNFTLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDIVNATGE  
LAWGVDETALQLEKVLHLYRSGQYLQNSTASSSTEYQCI PDSTIPQEDYRCWPSYHHGSC  
LLSVFNLAEAVDVCESHAQCRAFVVTNQTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226\_AA396601\_M

TRPGCAALRNVSGAQYVSGYTKAVYRVRLPGGAVALKAVDGSGHDLGSCVREFGARRG  
CYRLAAHKLLKEMVLLERLRHPNVLQLYGYCYQDSEIPDTLTTITELGAPVEMIQLLQTS  
SWEDRFRICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVNGELKVTDLDDARVEETPCT  
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDISI  
VNATGELAWGVDETALQLETAHLFRSGQYLQNSTSSRAEYQRI PDSAITQEDYRCWPSY  
HHGGCLLSVFNLAEAIDVCESHAQCRAFVVTNQTWTGRKL VFFKTGWNQVVPDAGKTTY  
VKAPG

SEQ ID NO: 227\_VRK3\_H

MISFCPDCGKSIQA AFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP  
KKVKWSSTVTS PRLSLFSGDSSSEEDTLSSSERSKSGSRPPTPKSSPQKTRKSPQVTR  
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLALPTGTVLTDKSGRQWKLKSFQTRDNQGI L  
YEAAPTSTLTCDSGPQKQKFSKLDAKDGRLFNEQNFFQRAAKPLQVNWKKLYSTPLLA  
IPTCMGFGVHQDKYRFLVLP SLGRSLQSLADVSPKHVLSERSVLQVACRLLDALEYLHEN  
EYVHGNTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFI SMD  
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGP CGH  
WIRPSETLQKYLKVVMA LTYEEKPPYAMLRNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228\_S71575\_M VRK3\_M

IPTCIGFGIHQDKYRFLVFP SLGRSLQSLADDDNPKHVVSERCVLQVACRLLDALEYLHEN  
EYVHGNTAENVFVN PEDLSQVTLVGYGFTYRYCPGGKHVAYKEGSRSPHDGDLEFI SMD  
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNT EKITRQKQKYLDSPERLVGL CGR  
WNKASETLREYLKVVMA LNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQMPV

SEQ ID NO: 229\_AA45427\_H

MGHALCVCSRGTVIIDNKRYLFIQKLGE GGF SYVDLVEGLHDGHFYALKRILCHEQQDRE  
EAQREADMHRLFNHPN IRLVAYCLRERGAKHEAWLLLPFFKRGTLWNEIERLKD KGNFL  
TEDQILWLLLGICRGLEAIHAKGYAHRDLKPTNILLGDEGQPV LMDLGSMNQACIHVEGS  
RQALTLDQWAAQRCTISYRAPELFSVQSHCVIDERTDVWSLGC VLYAMMFEGEPYDMVFQ  
KGDSVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQRPHI PLLLSQLEALQPPAPGQ  
HTTQI

SEQ ID NO: 230\_H05721\_H

MAVRQALGRGLQLGRALLRFTGKPGRAYGLRPGPAAGCVRGERPGWAAGPGAEP RRVG  
LGLPNRLRFFRQSVAGLAARLQRQFVVRAGWCAGPCGRAVFLAFGLGLGLIEEKQAESRR

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## FIGURE 1Z

AVSACQEIQAIFTQKSKPGPDPLDTRRLQGFRLEEYLIQSIGKGCSAAVYEATMPTLPQ  
NLEVTKSTGLLPGRPGTSAPEGQERAPGAPAFPLAIKMMWNI SAGSSSEAILNTMSQE  
LVPASRVALAGEYGAVTYRKS KRGPQLAPHNI IRVLRAFTSSVPLLP GALVDYDPVLP  
SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTSPRLAAMMLLQLLEGVDHLVQGGIAH  
RDLKSDNILVELDPDGC PWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVST  
ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFGQGAHLESRSYQEAQLPALPESVPP  
DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMVGWLLQQAATLL  
ANRLTEKCCVETKMMLFLANLECETLCQAALLCSWRAAL

SEQ ID NO: 231\_AI086865\_H  
MEKYERIRVVGRAFIVHLCLRKADQKLVIIKQIPVEQMTKEERQAAQNECQVLKLLNH  
PNVIEYYENFLEDKALMIAMEYAPGGT LAEFIQKRCNSLLEEETILHFFVQIILLALHHVH  
THLILHRDLKTQNILDKHRMVVKIGDFGISKILSSKSTPCYISP ELCEGKPYNQKSDIW  
ALGCVLYELASLKRAFEAANLPALVLKIMSGTFAPISDRYSPELRQLVLSLLSLEPAQRP  
PLSHIMAQPLCIRALLNLHTDGREVRGPQQHREQDHQCPLQGIIMTFGSGSNGCLGHGS  
LTDISQPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEPLSIDLGT AHSAAVTGEEDL  
GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPKCCWRHKQCTGHIIPFASDCV  
RHS LHLHSVNHCNCSRLKDSSSEDSSSRGAGPTCSHVIESPCFELTPEEEHVERFRYGW  
CKSYRPVSVAVIHHPLYHECGADDLNXXKRKRKRKRKRKSKPPIPTQVGPATASPDLTSMAT  
GTPDSTAPITIWRSSEPTGKGQGSKVIKKVKKKKEKEKDEEMDEKAKLKKKAKKGQLT  
KKSPVKLEPSPPDVSRSL SARQLARMSSESPESREELESEDSYNGRGQGE LSSSEDI VESS  
SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSNPNLS

SEQ ID NO: 232\_AA836348\_H  
MSVLGEYERHCDSINSDFGSES GCGDSSPGPSASQGPRA GGGAEEQEELHYIPIRVLGR  
GAFGEATLYRRTEDDSL VVWKEVDLTRLSEKERRDALNEI VILALLQHDNI IAYYNHFM  
NTTLLIELEYCNGGNLYDKILRQKDKLFEEEMVWYLFQIVSAVSCIHKAGILHRDIKT  
NIFLTKANLIKLDYGLAKKLNSEYSMAETLVGT PYYMSPELCQGVKYNFKSDI WAVGCV  
IFELLTLKRTFDATNPLNLCVKIVQGIRAMEVDSSQYSLELIQM VHSCLDQDPEQRPTAD  
ELLDRPLLKRKRSSSTVTEAPIAVVT SRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAG  
NTHFAVVTVEKELYTWVNMQGGTKLHGQLGHGDKASYRQPKHVEKLQGAIRQVSCGDDF  
TVCVTDEGQLYAFGSDYYGCMGV DKVAGPEVLEPMQLNFFLSNPVEQVSCGDNHVVLTR  
NKEVYSWGCGEYGRGLDSEEDYYTPQKVDVPKALI IAVQCGCDGTFLLTQSGKVLACG  
LNEFNKGLNQCMGSIINHEAYHEVPYTT SFTLAKQLSFYKIRTIAPGKTHTA AIDERGR  
LLTFGCNKGQLGVGNYKKRLGINLLGGPLGGKQVIRVSCGDEFTIATDEKVLNSKTIR  
SNSSGLSIGTVFQSSSPGGGGGGGGGEEEDSQESETPDP SGGFRGTMEADRGM EGLISP  
TEAMGNSNGASSCPGWLRKELENAEFIPMPDPSPLSAAFSESEKDTLPYEELQGLKVA  
SEAPLEHKPQVEASVTELF AFESQLVTSAESCSNLCWEGNTTDSSCVCVQLSAGG

SEQ ID NO: 233\_R86668\_H, MKK6\_H  
MNLLLSYRDVQDYSAILVELTQALPTCDVAEQHNVC FHYTFALNRRNRPGDRAKALSV  
LLPLVQLEGSVAPDLYCMCGRIYKDMFFSSGFQDAGHREQAYH WYRKAFDVEPSLHSGIN  
AAVLLIAAGQHFEDSKELRLIGMKLGCLLARKGCVEKMQYYWDVGFYLG AQIILANDPTQV  
VLA AEQLYKLNAPIWYLVSMETFLLYQHFRPTPEPPGGPPRAHFWLHFLLOSCQPFKT  
ACAQGDQCLVLVLEMNKVLLPAKLEVRGTD PVSTVTL SLLEPETQDIPSSWTFPVASICG  
VSASKRDERCCFLYALPPAQDVQLCFPSVGH CQWFCGLIQAWVTNPDSTAPAEAEAGAGE  
MLEFDYEYTETGERLVLGKGTYG VVYAGRDRHTRVRIAIKEI PERDSRFSQPLHEEIALH  
RRLRHKNIVRYLGSASQGGYLKIFMEEVPGGSLSSLLRSVWG PLKDNESTISFYTRQILQ  
GLGYLHDNHI VHRDIKGD NVLINTFSGLLKISDFGT SKRLAGITPCTETFTGT LQYMAPE  
IIDQGPRGYGAADIWSLGCTVIEMATGRPPFHELGSQAAMFQVGMVKVHPMPSSLSA

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## FIGURE 1AA

EAQAFLLRTFEPDPRLRASAOQLLGDPLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN  
 STTQSQTFFPCPQAPSQHPPSPPKRCLSYGGTSQLRVPEEPAAEEPASPESSGLSLLHQE  
 SKRRAMLAHVLEQELPALAENLHQEQKEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ  
 ELRALQGRRLAQGLGPALLHRPLFAFPDAVKQILRKQIRPHWMFVLDLSLRAVRAALG  
 VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR  
 EILAGKEREYQALVQALQRLNEEARTYVLAPEPPTALSTDQGLVQWLQELNVDSTIOM  
 LLNHSFTLLTYATRDDLIYTRIRGGMVCRIWRILAQRAGSTPVTSGP

SEQ ID NO: 234\_PAK6\_H

MFGKKKKKIEISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT  
 PIQLAPMKTIVRGNKPKCKETSINGLLEDNIVSVTRNSLRKESPTPDQGASSHGPCHA  
 EENGFITFSQYSSSEDTTADYTTEKYREKSLYGDDLDPPYRGSHAQNGHVMKMKHGEA  
 YYSEVKPLKSDFAFSADYHSHLDSLSKPSEYSDLKWEYQRASSSSPLDYSFQFTPSRTA  
 GTSGCSKESLAYSESEWGPSLDDYDRPKSSYLNQTSPOPTMRQRSRSGSGLQEPMPFG  
 ASAFKTHPQGHSYNSYTPRLSEPTMCIPKVDYDRAQMVLSPLSGSDTYPRGPAKLQPS  
 QSKSGYSSSSHQYPSGYHKATLYHHPSLQSSSYISTASYLSSLSLSSSTYPPPSWGSSS  
 DQQPSRVSHEQFRAALQLVVSFGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM  
 DLRKQQRRELLFNEVIMRDYHHDNVDMYSSYLVDDELWVMEFLEGGALTDIVTHTRM  
 NEEQIATVCLSVLRALSYLHNQGVHRIKSDSILLTSDGRIKLSDFGFCQVSKEVPKR  
 KSLVGTPYWMAPVISRLPYGTEVDIWSLGMVIEIMIDGEPYPFNEPPLQAMRRIRDLSL  
 PRVKDLHKVSSVLRGFLDLMLVREPSQRATAQELLGHPFLKLAGPPSCIVPLMRQYRHH

SEQ ID NO: 235\_SURTK106\_H

MNDRNEIQMEAKLQSLTIIAQEILCRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI  
 LCGPSREGDSPVAMGMTRMLLECSLSDKLCVIEKQYEVIIIVPTLLVTIFLILLGVILWL  
 FIREQRTQQQSGPQGIAPVPPRDLSEAGHGNNVALPLKETSVENFLGATTALAKLO  
 VPREQLSEVLEQICSGSCGPIFRANMNTGDPSKPKSVILKALKEPAGLHEVDLGRIFQ  
 HQYLGHKKNLVQLEGCCTEKLPLYMVLEDVAQGDLLGLWTCCRDMTMDGLLYDLTEKQ  
 VYHIGQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT  
 IPLKWLAPERLLLRLPASIRADVWSFGILLYEMVTLGAPPYEPVPTSILEHLQRRKIMKR  
 PSSCTHTMYSIMKSCWRWREADRPSRELRLRLLEAAIKTADDEAVLQVPELVPELYAAV  
 AGIRVESLFYNYSML

SEQ ID NO: 236\_AA098024\_M

LQEKHLFHGDVAARNILIQSDLTPLKCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL  
 LRPASIRGDIWSFGILLYEMVTLGAPPYEPVPTSILQYLQRRKIMKRPSSCSHAMYNIM  
 KCCWRWSEDSRPLLQVLLQRLLEAASRSADDKAVLQVPELVPELYADVAGIRAESISYSF  
 SVL

SEQ ID NO: 237\_SGK2ALPHA\_H

MNSSPAGTPSPQPSRANGNINLGPSANPNQAQPTDFDFLKVIGKGNYGKVLLAKRKSDGAF  
 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE  
 LFFHLQRERRFLEPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTDGFL  
 CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDQVS  
 QMYENILHQPLQIPGGRTVAACDLLQSLHKKDQRLGSKADFLEIKNHVFFSPINWDDL  
 YHKRLTPFPNPNVTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE  
 DDDILDC

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## FIGURE 1BB

SEQ ID NO: 238\_CCRK\_H  
MDQYCILGRIGEGAHGIVFKAKHVETGEI IALKKVALRRLEDGFPNQALREIKALQEMED  
NQYVVQLKAVFPHGGGFVLAFAEFMLSDLAEVVRHAQRPLAQAVKSYLQMLLKGVAFCHA  
NNIVHRDLKPANLLISASGQLKIADFGLARVFS PDGSRLYTHQVATRSVGCIMGELLNGS  
PLFPGKNDIEQLCYVLRILGTFNPQVWPELTEL PDYNKISFKEQVPMPL EEVLPDVSPQA  
LDLLGQFLLYPPHQRIAASKALLHQYFFTAPLPAHPSELPI PQR LGGPAPKAHPGPHIH  
DFHVDRPLEGVAVEPRADSALHPGGVRSWPWSRLPAPQDHSVHLFLCHLPGFTLQGLPMA  
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS  
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239\_TESK2\_H  
MDRSKRNSIAGFPFPRVERLEEFEGGGGEGNVSQVGRVWPSSYRALISAFSRLTRLDDFT  
CEKIGSGFFSEVFKVRHRASGQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINSG  
NLEQLLDSNLHLPWTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNCLIKRDENGYS AVVA  
DFGLAEKIPDVSMGSEKLAVVGS PFWM APEVLRDEPYNEKADVFSYGI ILCEI IARIQAD  
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLT FNCCNMDPKLRPSFVEIGKTL EEILSRL  
QEEEEQERDRKLQPTARGLLEKAPGVKRLSSLDDKI PHKSPCPRRTIWLSRSQSDIFSRKP  
PRTVSVLDPYYRPRDGAARTPKVNPFSARQDLMGGKIKFFDLPSKSVISLVFDLDAPGPG  
TMPLADWQEPLAPPIRRWRSLPGSPEFLHQEACPFVGREESLSDGPPPRLLSSLKYRVKEI  
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEERPAGSTPATF  
STSGIGLQTQ GKQDG

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## FIGURE 2A

SEQ ID NO: 1\_X69117\_H BARK2\_H

ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCACTTACCTGATGGCCATGGAGAAGAGC  
AAGGCGACCCCGGCCGCCCGCCAGCAAGAGGATCGTCCTGCCGGAGCCCAGTATCCGG  
AGTGTGATGCAGAAGTACCTTGCAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT  
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTTGTTTGAATGAAATTAATGAAGCTGTA  
CCTCAGGTGAAGTTTATGAAGAGATAAAGGAATATGAAAACTTGATAATGAGGAAGAC  
CGCTTTGCAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACCTTTCTTCTGT  
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA  
GTGACATCAACTCTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC  
ATTTTTCAAAAATTTATGGAAAGTGACAAGTTCAGTAGATTTTGTGAGTGGAAAAACGTT  
GAATTAAATATCCATTTGACCATGAATGAGTTCAGTGTGCATAGGATTATTGGACGAGGA  
GGATTCGGGGAAGTTTATGGTTGCAGGAAAGCAGACACTGGAAAAATGTAATGCAATGAAA  
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA  
ATCATGTTGTCTCTTGTGACAGCAGGAGACTGTCTTTCATTGTATGTATGACCTATGCC  
TTCCATACCCAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGGATTTGCAC  
TACCACCTTTTCAACAACACGGTGTGTTCTCTGAGAAGGAGATGCGGTTTTATGCCACTGAA  
ATCATTTCTGGGTCTGGAACACGTGCACAATCGGTTTGTGTCTACAGAGATTTGAAGCCA  
GCAAATATTCTCTTGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCTGC  
GATTTTTTCCAAAAGAAGCCTCATGCGAGTGTGGCAGCCATGGGTACATGGCTCCCGAG  
GTGCTGCAGAAGGGGACGGCCTATGACAGCAGTGCCGACTGGTTCTCCCTGGGCTGCATG  
CTTTTCAAACCTCTGAGAGGTCACAGCCCTTTCAGACAACATAAAACCAAAGACAAGCAT  
GAAATTGACCGAATGACACTACCGTGAATGTGGAACCTTCAGACACCTTCTCTCCTGAA  
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTCAC  
GGAGGCGGCTCACAGGAAGTAAAGAGCACAGCTTTTTCAAAGGTGTTGACTGGCAGCAT  
GTCTACTTACAAAAGTACCCACCCTTGATTCTCTCCCGGGGAGAAGTCAATGCTGCT  
GATGCCTTTGATATTGGCTCATTTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT  
TGCGACCAAGAACTCTACAAGAACTTCCCTTTGGTTCATCTCTGAACGCTGGCAGCAAGAA  
GTAACGGAAACAGTTTATGAAGCAGTAAATGCAGACACAGATAAAATCGAGGCCAGGAAG  
AGAGCTAAAAATAAGCAACTTGGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT  
ATGCACGGGTACATGCTGAACTGGGAAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT  
TTTTACCTCTTTCCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA  
CTGACAATGGAACAGATTCTCTCTGTGGAAGAACTCAAATTAAGACAAAAAATGCATT  
TTGTTTCAATAAAAGGAGGGGAAACAATTTGTCTTGAATGTGAGAGTGATCCAGAGTTT  
GTGCAGTGGAAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCAGCGGCTATTGCGTCTGT  
GCCCCGAAGTTCCTCAACAAACCTCGGTACAGGTACTGTGGAGCTCCCAAAGCCATCCCTC  
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2\_AA144574\_M BARK2\_M

CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA  
CGTGAGGATATCGGATCTCGGCCTTGCTGTGATTTCTCCAAAAGAAGCCTCATGCCAG  
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAACGTGCTATGACAG  
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACCTTCTGCGGGGCCACAGCCC  
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCTGACCGTGAA  
CGTGCAGCTTCCAGATGCCTTCTCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGCTCCA  
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGAGGGGCACGAGAGTTGAAGGAGCA  
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTACTTACGGAAGTACCCGCCACCCCT  
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCTTCGATATCGGCTCCTTCGATGA  
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC  
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGGAGACCATCTATGACGCCGTCAA  
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

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## FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA  
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTACCTGTTCCCAACAGACTGGAGTG  
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA  
GGAGACCCAGATTAAAGACAGAAAGTGCATCTTAGTCAGGATAAAGGGAGGGAAGCAATT  
TGTCTTGCAATGTGAGAGTGACCCCGAGTTTGACACAGTGGCTGAAGGAGCTGACCTGCAC  
CTTCAATGAGGCCAGAGACTGCTGCGCCGTGCCCCAAATTCCTCAACAAACCACGGGC  
CGCCATCCTGGAGTTCTCCAAGCCACCACTGTGTACAGAAATAGCAGCGGCCTCTGAAC  
CACAGAGCAGCGGGGCCTGAAGGAGGGGCCAGCTCTTCAGCCCAGGAGTGGAACGAAG  
CCACGGGGAACCGTGTGGGGCTAAGACACAGTGTCTGAGCACTGACGGGGCTGCTCCA  
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG  
TCCTATCCCACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3\_AA826850\_H  
GAAGAGGATGGGCTCGTCCATGTCGGCGGCCACCGCGCGGAGGCCGGTGTGTTGACGACAA  
GGAGGACGTGAACTTCGACCACTTCAGATCCTTCGGGCCATTGGGAAGGGCAGCTTTGG  
CAAGGTGTGCATTGTGCAGAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA  
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCGGGAGCTGGAGATCCT  
GCAGGAGATCGAGCACGTCTTCTGCTGAACCTCTGGTACTCCTTCAGGACGAGGAGGA  
CATGTTTCATGGTGTGACCTGCTACTGGGCGGGGACCTGCGCTACCACCTGCAGCAGAA  
CGTGCACTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA  
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA  
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGA  
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGGAGATCTTCCAXTCTTT  
TGTCACGGCGGGGACCGGCTACTCCTTCGAGGTGGACTGGTGGTGGGGGTGATGGC  
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC  
CCTGGTGCAGCTGTTTCAGCACCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT  
GGACGTGCAGGCAGCCCCGGCGCTGGCCGGCGTGCTGTGGGACCACCTGAGCGAGAAGAG  
GGTGGAGCCGGGCTTCGTGCCCAACAAAGGCCGTGCTGCACTGCGACCCACCTTTGAGCT  
GGAGGAGATGATCCTGGAGTCCAGGCCCTGCACAAGAAGAAGAAGCGCCTGGCCAAGAA  
CAAGTCCCGGGACAACAGCAGGGACAGCTCCAGTCCGAGAATGACTATCTTCAAGACTG  
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTAAACAGAGAAAAGCTGAAGAGGAGCCA  
GGACCTCCCGAGGGAGCCTCTCCCCGCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA  
GGACGAGGCGGAACGCTCCGCCCTGCCCATGTGCGGCCCATTTGCCCTCGGCCGGGAG  
CGGCTAGGCCGGGATGCCCGTGGTCTCACCCCTGAGCTGCTTTGGAGACTCGGCTGCC  
AGAGGGAGGGCCATGGGCCGAGGCCTGGCATTACAGTTCACCCAGCCTGGCTGGCGGT  
GCCCCAGTGCCCCGGACACATTTACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG  
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGGAGCTGGGGCCATGGATG  
GGACAGGAGTCTTTGTCCCTGCTCAGCCCCGAGGCTGTGCACGGCCCTCGTCACAAGGTG  
ACCCTTGACAGCAGGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCTTGGAGGTCAAGGGC  
ATGGGTTGGGGTAGTGGGTGGGGAGGTGAATGTTTTCTAGAGATTCAAACCTGCTCCAGCA  
ATTTCTGTATAGTTTTACCTCTGAGAATTACAATGTGAGAACCCTC

SEQ ID NO: 4\_AA960957\_H  
GTCCACATCCCGCATCCGGCATCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG  
GAATATGGGCGGGAACCACTCCCAAGCCCCCGTGTGTTGACGAGAATGAGGAAGTCAA  
CTTTGACCATTTTTCAGATTCTCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT  
CGTGCAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG  
CATCGAGAGGGATGAGGTTCGGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

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FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTTCATGGT  
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTCCAC  
AGAGGGGACTGTGAAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG  
GTACCACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACA  
TGTTTCACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTC  
CATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGG  
CCCCGGATACTCGTACCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT  
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCCATCGATGAAATCCTCAACAT  
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT  
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG  
CGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGCACTGATGCCCGG  
CTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCACATTTGAGCTTGAAGAGATGAT  
TCTAGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGA  
TGGCACAAGGACAGCTGCCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG  
GGAGGAATTCATCATATTCAACAGAGAGAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA  
GCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCTCCAGGACGGGTG  
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCACACTTG  
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCTCTTTGTGC  
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGA  
GCTGGGAAGCCTGGGTTCTGGTCCCCTCTCCATGACTGATTCACGTGTGACCTCAGACAA  
GTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTTAAACACTTCTGCC  
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAAACCTT  
TGATATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC  
ATTCCCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCAGATCCTAGCTTGTAGA  
GGGCACTTCCGAAAAACACAGCCCTGACAGCAAAATAAAGGTCTGATATGTTGGCCCTT  
CTATGGAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT  
CTGGCAGGCCACAGTCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC  
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCTCATTTAAGAAGACTATCCTTACCTTTT  
AGTTTCAGCAGTCTCACCACCACATATCCCCAGTGCTGGGATGGCACACAGGTGTCCA  
TTCAGATGAGAGTTGGGTGCGCTGAGCATTGGTTACTCCTGCAGAGTGAATCAGCACCCC  
ATCCAACCTGGCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAACCTCTATCAGCTTTC  
AGGGTTTTCTCTCCTGGGAAGGGTGTAATAATCAGCTTGTGAGATTCTTCTTACAGAGAGT  
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG  
AAAGTTTATTTTCAAGGAGGAAAAATGGGTTACACAAAAAGCAAACTACATTCTGATCTGCT  
CAGGGAGAAGCTTGCCTTTGAACTGGAAGATGTTGGGATGAGCAGGGAAAGCTTAGACTT  
TGGAGTCAGGTTTGTGTTTCAGAATCCAGCCCTGCTGGCTACTAACTAAGTGGGAGACCTT  
AGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCTCTATTTTAAACAGGGATAATAAA  
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG  
GATGACTCATAGAAATGGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTC  
TTCCTTCACTCACCCAGCAGGTGAGTTTTCTGTGCAAAACAACTGTTTAGGATTCTTCC  
AAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGCTGAAGTTCGACTGTG  
TTTTTATTTTTTTCATCCAACCTCCATTTTTTCACTTTTACATGATTACTCAATCCTTGGG  
GCTGTCCATGTCATCTCTTAGATTTCTTAAAGACATTTTAATGTATGGTTAGGTTTTAT  
ATTTTTATTTTTTAAAAAAGAAATAGTCAGTGTTTTCTCCTTTCAACCGAGACTATTTTC  
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTTTTGCACTTTTCTTTACTTCATGTCCC  
CATCAACAACCGTCTGCTCCCCACCTCCCCAGGAAATAAGGGGCTGCTCCTCTCCCT  
ACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGA  
ATTAGGGGACAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTCTGTTCAAGT  
TGGCATTTCTGTTTGGAAATAAATATTCTTGGACATTCCTTC



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## FIGURE 2D

SEQ ID NO: 5\_TBK1\_H  
TCCTGAGTCTCGAGGAGGCCGCGGAGCCCCGCCGGCGGTGGCGCGGCGGAGACCCGGCTG  
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC  
TTTTATCTGATATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA  
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG  
ATGTTCAAATGAGAGAATTGAAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAAAT  
TATTTGCTATTGAAGAGGAGACAACAAGACATAAAGTACTTATTATGGAATTTTGTCTC  
CATGTGGGAGTTTATACACTGTTTTAGAGAACCTTCTAATGCCTATGGACTACCAGAAT  
CTGAATTTCTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG  
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC  
AGTCTGTGTACAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT  
TTGTTTCTCTGTATGGCACAGAAGAATATTTGCACCCCTGATATGTATGAGAGAGCAGTGC  
TAAGAAAAGATCATCAGAAGAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA  
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA  
ATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC  
AGAAAGCAGAAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTCTTGCAATCAGG  
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAAACATCCTTGAAGCAGATCAGG  
AAAAGTGTGGGGTTTTGACCAGTTTTTTGCAGAAACTAGTGATATACTTCACCGAATGG  
TAATTCATGTTTTTTTCGCTACAACAAATGACAGCTCATAAGATTTATATTCTCAAATC  
ATACTGCTACTATATTTTATGAACCTGGTATATAAACAACCAAAATTTCTTCAAATC  
AAGAACTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACAT  
TCCCTAAAACCTACTGAGGAAAACCTATATTTGTAGTAAGCCGGAACCTCTGAATACCA  
TAGGATTAATATGAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG  
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAAATGGCA  
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTA  
TTAAAGATGATTACAATGAACTGTTCAAAAAAGACAGAAGTTGTGATCAATTGGATT  
TCTGTATCAGAAACATTGAAAAAAGTGTGAAAGTATATGAAAGTTGATGAAGTCAACC  
TGGAAAGCGGCAGAGTTAGGTGAAATTTTCAAGATATCGACAGCAGATTATCTCCAGGTG  
GTTCTCAGGGAAACAATAGAAACAGTCTTCAAGATATCGACAGCAGATTATCTCCAGGTG  
GATCACTGGCAGACGCTGTTAAATTCAGTATGACAGAGATTACTATCAGTTCAAAAAAGACA  
AAAAACTACAAGTCTGTTAAATTCAGTATGACAGAGATTACTATCAGTTCAAAAAAGACA  
AAGCAGAACGTAGATTAGCTTATAATGAAGAACAAATCCACAAATTTGATAAGCAAAAAAC  
TGTATTACCATGCCACAAAAGCTATGACGCACTTTACAGATGAATGTGTGTTAAAGTATG  
AGGCATTTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCACTTTAGGAAACAGT  
TATTATCGCTGACTAATCAGTGTGTTGATATTGAAGAAGAAGTATCAAAATATCAAGAAAT  
ATACTAATGAGTTACAAGAACTCTGCCTCAGAAATGTTTACAGCTTCCAGTGGAAATCA  
AACATACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGTA  
TGAAGAAATTAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAAAACCACA  
TTTGTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTTGACTGTCTTT  
AGCTTTCTAATAGAAGTTTAAAGAAAGTTTCCGTTTGCACAAGAAAAAACCCTTGGGCA  
TTAAATGAATGCCTTTATAGATAGTCACTTGTCTTCTACAATCCAGTATTTGATGTGGTCG  
TGTAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTGGCTGCTGTGAA  
GATGTAATTTTATCTTTTAACTTTATAATTATATGAGGAAATTTGACCTCAGTGATCAC  
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTTACTCTGAGTGGGGC  
TAAATAAGTTATTTTCTCTGACCGCTACTGGAAATATTTTAAAGTGGAAACCAAAATAGG  
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTGTAAATGGTAGAACGGTGGCTAC  
TGTGAGTGGGGAGCAGAACCGCACCCTGTTATACTGGGATAACAATTTTTTGAAGG  
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCAGATCCAGTTATCCTTGTATCCATG  
TAATTTTCAGATGAATTATTAAGCAACATTTTAAAGTGAATTCATTATTAATAAACTATT  
ATTTTTTCTTTGGCCATAAATGTGTAATTGTCAATTAATTTCTAAGGTCAATTTCAACT

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## FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTTCATGGAAAAAATAAATTTCT  
CAATTTTAAAAAA

SEQ ID NO: 6\_AA305176\_H

TGGCTGCTCGCGGAGGGGCGAGTGTACGCGGGGCGGCTGTAGGCTGTCCAGCGATGGATCC  
CACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAG  
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTCAGCATAGTGAAGCCCATTAGCCG  
GGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTTGTATGCAGTAAAGGT  
TGTTAAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA  
TGCACTGGCACTAAGCAAAAGCCCATTTCATTGTCCATTTGTATTATTCAGTGCAGTCTGC  
AAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCCTACA  
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC  
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT  
TATTTCTAATGAGGGTCATATTAACTGACGGATTTTGGCCTTTCAAAAGTTACTTTGAA  
TAGAGATATTAATATGATGGATATCCTTCAACACCATCAATGGCAAAACCTAGACAAGA  
TTATTCAAGAACCCAGGACAAGTGTATCGCTTATCAGCTCGTTGGGATTTAACACACC  
AATTGCAGAAAAAATCAAGACCTGCAACATCCTTTCAGCCTGTCTGTCTGAAACATC  
ACAGCTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGACACTACGCCTTA  
TTCTAGCAAATTAATAAATCATGTCTTGAAACAGTTGCCTCCAACCCAGGAATGCCTGT  
GAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG  
TAGTCAATCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAAATG  
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA  
AATGAATGTGAGAAATATTATACCTTTTCATATAAATTCATAAAGAAATGAAATTGTTA  
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCTGACATTCTGTCAAATTC  
TTTTGAAATATTTCAATTTCTCATTCAATTGTGACATTGTTCTTACTTGATTATATAATGA  
GATTCTTGCAATAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT  
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTGTTTGTGTTTATTTTGT  
TTTAAACATATGTCAATTTAAAACTCATATTACCTCCTTTT

SEQ ID NO: 7\_AA116841\_M

CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG  
CAATGGACATGCTTTTAACCATTTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAC  
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTCCG  
TACCCCAACAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC  
ATCTGACCGTATCTGGGTTAGTCTGTAGCACATGCGTGTCAATTTTATCTAACTTGTGA  
TATAGAATTAAGTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA  
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAATTACTAAGTACAACAGTTTTTACAG  
AATTAAAACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAACTGTATATAA  
GCCATAATAGCTTTTTTTCATCTTATTTCACTGCACTTTATGAAGAGCAAAGTATCAA  
TAACTAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8\_AA256100\_H

AGGGAGCTGACGGGCGCCCGGCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCCGCGGGC  
GCGACCGGAGGCGAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC  
TATGAGCAACCATACCCGGGAAAGAGTGACTGTAGCCAAGCTCACATTGGAGAATTTTAA  
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAACCAGGCAGAAGAAATAGAAGTGGC  
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAGAAAAGTTACGTGATCACAACAGCTCG  
CAAAGAAACAGAGTTCTTACGGCTCAAAGGACCAGACTTGGCTTGGATGACTTTGAGTC  
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC  
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAGAGCAGGT



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## FIGURE 2F

GGCCCATATCCGAGCAGAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA  
GATGTTTTTACAGTTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG  
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT  
CTACATTTTCAGAGACTGTTCTGGCAATAGATGGGATCCACCAGTTGGGTTTTATCCATCG  
GGATATTAAGCCAGACAACCTTTTATTGGATGCCAAGGGTCATGTAAATTATCTGATTT  
TGGTTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTATAGAAATCTCACACA  
CAACCCACCAAGTGACTTCTCATTTCAGAACATGAACTCAAAGAGGAAAGCAGAACTTG  
GAAGAAGAACAGGAGACAACCTGGCATATTCACAGTTGGGACACCAGATTACATTGCTCC  
AGAAGTATTCATGCAGACTGGTTACAACAAATTGTGTGACTGGTGGTCTTTGGGAGTGAT  
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA  
CAGAAAAGTGATGAACTGGAAAGAACTCTGGTATTTCTCCAGAGGTACCTATATCTGA  
GAAAGCCAAGGACTTAATTCTCAGATTTTGTATTGATTCTGAAAACAGAATTGGAAATAG  
TGGAGTAGAAGAAATAAAAGGTCACTCCCTTTTTTGAAGGTGTGCGACTGGGAGCACATAAG  
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAGCATTGATGATACTTCAAATTTTGA  
TGACTTCCCTGAATCTGATATTTTACAACAGTGCCAAATACCACAGAACCGGACTACAA  
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG  
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA  
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC  
TGAAATACTCCTGAAGATGGTGGTGCTTATTGACTACAAGAGGAAATCTACAGGATTAG  
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTAAATAT  
TTTATTATTTTTGTAACTTTATTATATGAAGGTACTGGAATAAAAGGAACAGACATCCC  
TTTCTAACTGCACTGCCTACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT  
TTGAACTGTAAACACCTCTAATCAATTCAGGAGAAAACACATATCATTTAAAGCAACATAGG  
CTAACCTGTAGGTAACTGCACTGAGTATTGATGTTTTACTGCAAATCTTATGGGTCTAGATA  
ATCAGTAAAAGCCATCTTCCATAGTTGGTGTGTAACATTGCCCTATTGGTTTGGACATC  
TGTAAGATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAGAAATTCACAGTAAGGAG  
CTGGTTCTTTACAAAATAGAATTTATCATCAAGTTATTACACAACTTCACAGTAAGGAG  
TGACAAGTTTTATAAAGGAAGACAAAGTTTTAACACCTTCACTCAAGCACTCCACTAATA  
TATTTACGTTGCATTACAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG  
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTCTTGTGACAAGAGAATCTTCTT  
TTTTTAAACAAGAGGACATGGCATTATTTTAAATTTGATTATGGTGAGTTGAATTTAAGACA  
TGACCATGAAGGCTGCTTGTAGAATTAGTGTATTTTATTAACTATTTTTTTAAATGTC  
AACTTCTATCATGTAAATGGACTTATAGAGAACAAAAGCTATTTACTTTGGTTTTCTA  
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTATTTCTTTTGATGAAAATTTTCTCTT  
TGATAGTACTTGTATTATTGTGCCATTATTTCTTATGCTCCAAATGTACCAAGATCTT  
GAACAGAGTGGATGTTCACACTGAGTAGAATTTTCTTCTGCTGGGCATGCTGTATTG  
AGACCTGACAGATCTTTGATAGAGGTGAGCTTATTAAAGGGCAATATTGTTCTTGTATTG  
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGGTTGT  
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATTCTTGGGTATCTCTCTAAGAATT  
AAATAATCTTTTCTAGCTTAATATTTTAACTTCTAATTCAAACAACCTCTGAGGTTTTGGTT  
TCATTAGTAATAGTTGAGGAATAATATACTAGCAAAGAATGGCCTAATGTTTGTACATAAC  
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATTATAAATGATCTATGA  
TCAAATCTAAAGTGATGAATTATTGTAGGAATGTCTTCTAATGGGGAAGAATTGCAT  
AGGAGCATTATGCAAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG  
TGTTTTATAAGGCCATCCTGTTCCCCCAACTCCCCCATTTTGGTTTTGTTCTTTTTAA  
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCACTTCCATTTTTCTAGTCTGGAT  
TTTTTGAGTATTTAGGAAAGAGAGCTATTAAAACTCTGGGGATTTCTCAATGTGACTAA  
CTCTAATTTTTCTAATTATACTGCCTTTAATTAACATAATATTAATTTTGCTGAGGT  
TATGAGATTTTCTACCCACATCGCTCCCCTTTTTTAAAGGAGTGTCTGCTAGTG  
TGATAATGAATAGGTAAGATATGAGATAATTGCAACATTGTCTAGTCTAGTATGGTAA

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FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA  
GAAACTGATTTACCTAAGTTTACTTTTAAATTGCATAATAGAGCATTTTTTGTGTTTGAGT  
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTACTTTCTTGGAAGTGAAG  
GGTAGTTCTGGAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA  
TTCACAATCTTTGGGGTTTTCTCCTCATCAAAGCATTCTTAAGTGCCTATCTAAAAGC  
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTTCATGATGCAAATTAAGT  
AGATAATTTGCAAAGTACCTTGAGATTGAATTTTCTCTATTATATATTTCCCATATTTTC  
AGGTGAATAATTTAATTTAAATGACAAAACCTATCTAGTCAACTGGGCATAATGACATT  
TTCTTTAAATTAGACTCTATTTTGAATTAAAAGAGTTTTATTATAAACCGTGTGTTTTTG  
GTTTTTCTAAGTATATAGAAAGCTTGTATAATTCAGATTTATCAATTTCTGATTTAATG  
TAGACTTTGACTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTCTTTT  
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTGTGCTGTCT  
GAAAATAAGGAATTGCTTATAAACAGCCACTTCTGAATACAATATGTAGCTGATTTAAT  
AAGCTAGTTAGTGAATGGAATAAGTGTGGAGTATTAAAAATGTTCTTTGGTTGGTAAG  
GCCTAAGATAGGGTTTCATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT  
TTTATGTAAATCTCTAAATTTAAAATATTTTAAAGTACATTTATTTTGGTGTGTTTTATTGT  
ATAAACCTTAGACAATCAATCAGTCAGTCTTTACTGACAGGAGCAGCAGCTATCTGTCT  
TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA  
ACACATTCTCCTTTGAATTGTTAAAATTCAGAACATTCAAATAACTGTTTTGCTACAAC  
CCATGATTATTTTCTGTTGTGTTTATTTAAATTTACTTTCTCTTTAGAAGTGCACATTAT  
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGGA  
CTACTAGAGATATTTTAGATTTTTATGAAAAAATGTGAGGGGATATTGCTGCTTTAAAA  
AGGAATAAAGTAATAAAAAATATATCTCAGCTATTTTTTTAAAGCAATATAATTAGCAAT  
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTCAGTTACTGAGTTTCAAAAA  
TGTTTTGGTGGCATGAGGACAAAATTTCAATTGAAGGTAAGATAAGAATAAAAACTATGTT  
TAC

SEQ ID NO: 9\_AA210825\_H

CACGAGGGCTACTGGCGCCTGGCGACCCCTCCCTGCCCCCACCACCCCGCTCCGGCAA  
CGCCCCCTTCTCAGGCTCCCGACCGAATTTTCTCCAATTTCTGCGACTCGTGAGATT  
CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCCATCCCTGGCCGGTCCGGTCCC  
TGCGAACCCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA  
CCCCCAAGGACCCCGCCATCCTCAGGTCCCTCCGCTGCCAGATCTTTTCTCGGATCCC  
CGCTCTCCACCACCTGCTCAGAGATCCCGCGGATCTAGAACCCAGGGTCCCCCGGGC  
CCCCCGGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCCGGCCTCCCCCATGGCCAC  
CGCCCCCTCATTATCCCGCCGGGCTCCCTGGCTCTCCCGGGCCGGGGTCTCCTCCGCCCC  
CCGGCGGCCTAGAGCTGCAGTCGCCGCCACCGCTACTGCCCCAGATCCCGGCCCGGGTT  
CCGGGGTCTCCTTTACATCCAGATCGGGCTGACCCGCGAGTTCGTGCTGTTGCCCGCCG  
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGAGGACAGAAGTTCCTTG  
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTTCAAACATGACCCACGTCGG  
CCAACCTCCTGCAGCTGGTGCCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG  
TGGTGTGCTCGGCCTCGGCCACCTTCGAGGACTTCAGATCCGCCCCGACGCCCTCACGG  
TGCACTCCTATCGGGCGCCTGCCTTCTGTGATCACTGCGGGGAGATGCTCTTCGGCCTAG  
TGCGCCAGGGCCTCAAGTGCGATGGCTGCGGGCTGAATACCACAAGCGCTGTGCCTTCA  
GCATCCCCAACAATGTAGTGGGGCCCGCAAACGGCGCCTGTCTATCCAGTCTCTGGCCA  
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA  
GCCGTAGCACACCGAACTCCTGCCTCGCCGTCCCCGTCTATCCTCTTCTCTCTCTG  
CCTCATCGTATACGGGCCGCCCATTTAGAGCTGGACAAGATGCTGCTCTCAAGGTCAAGG  
TGCCGCACACCTTCTCATCCACAGCTATACGGGCCACCGTTTGCCAGGCTTGCAAGA  
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC

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## FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGGAGGCCCTTATCAATGGAG  
ATGTGCCGATGGAGGAGGCCACCGATTTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG  
AGTCAGAGGACTCCGGTGTTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG  
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCAGAGCTCCCTGGGGTACATCCCCCTAATGA  
GGGTGGTGCAATCGGTGCGACACACGACGCGGAAATCCAGCACCACGCTGCGGGAGGGT  
GGGTGGTTTATTACAGCAACAAGGACACGCTGAGAAAGCGGCACTATTGGCGCTGGAGT  
GCAAGTGTATCAGCTCTTCCAGAACAACGACCAACAGATACTATAAGGAAATTCGCG  
TGTCAGAAATCCTCAGGTGGAGTCCGCCCAGAACTTCAGCCTTGTGCCCGCCGGGCACCA  
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG  
GCGGGACTCCGGGTGGGCCAAGTGGGCAGGGGGCTGAGGCCGCCCGGGGGCTGGNNGAGA  
CAGCCATCCGCCAGGCCCTGATGCCCGTCATCCTTCAGGACGCACCCAGCGCCCCAGGCC  
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA  
ATGTGGACATTGCCACTGTCTACCAGATCTTCCCTGACGAAGTGCTGGGCTCAGGGCAGT  
TTGGAGTGGTCTATGGAGGAAAACACCGGAAGACAGGCCGAGCTCCGGAATGAAGTGAAGTCA  
TTGACAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCCATTC  
TGCAGAGCCTGCGGCATCCCGGGATCGTGAACCTGGAGTGCATGTTTCGAGACGCCTGAGA  
AAGTGTCTTGTGGTGATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG  
AGAAGGGCCGGCTGCCTGAGCGCTCACCAGTTTCTCATCAGGATGATCCTGTCCAGTG  
TGAGACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAACACAGAAAACGTGTTGC  
TGGCATCAGCAGACCCATTTCCCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA  
TCGGCGAGAAAGTCGTTCCGCCGCTCAGTGGTGGGCACGCCGCTACCTGGCACCCGAGG  
TGCTGTCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCAGTGGCGTGATCATGT  
ACGTCAGCCTCAGCGGCACCTTCCCTTCAACGAGGATGAGGACATCAATGACCAGATCC  
AGAACGCCGCTTTCATGTACCCGCCAGCCCTGGAGCCACATCTCAGCTGGAGCCATTG  
ACCTCATCAACAACCTGCTGCAGGTGAAGATGCGCAAACGCTACAGCGTGGACAAATCTC  
TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA  
AGATGGGAGAGCGATACATCAGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGCAG  
CAGAGCATCCGCTGCCTGGGTCTGGGCTGCCACGGACAGGGATCTCGGTGGGGCCTGTC  
CACCACAGGACCACGATGCAAGGGCTGGCGGAGCGCATCAGTGTCTCTGAGGTCTCTG  
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGTTCTTACAGGATCCAGCAATGAACTG  
TTCTAGGGAAAGTGGCTTCCCTGCCCAAAGTGGATGGGACACGTGGGGAGTGGGGTGGGG  
GAGCTATTTCCAAGGCCCTCCCTGTTTCCCAGCAATTAACGAGTCACTCTGCCC  
CCATGGCCTTGATCTCAGCAAAA

SEQ ID NO: 10\_AA127299\_H  
ATTCAATTCATAATTGTTGGTGCAAAAGATTTGCTTGCTATGGATTCAAATGGTCTTTCT  
GATCCTTACATCAAAATCACAATCTTTCTCAAAAAACGAAAGTGATTAAGAAAACTTTG  
ACTCCAATTGGAATGAACTTTTTTGTGCATTTTCCAGAAAAACAACCTTGAATTA  
GAATGTTGGGACCAGATACTTTTTTTCAGATGATTTTATGGCAAGGCTTCCATTTCTTG  
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAAAGAAAAAGGA  
GAATTTGCAGGAAAA

SEQ ID NO: 11\_AA316804\_H  
ATGTCTGCAAATAATTCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCTT  
GCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCTTAAGACGGGACTCTCTGCCCGACTC  
TCTAATGGAAGCTTCAGTGACCATCACTCACCAGGCTCAGTGACATACAGTT  
TCATTTCTACTGCAAATTGGCCTCACACGGGAGAGTGTACCATTGAAGCCCAGGAACTG  
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT  
GGATTCTTTGGCATGTATGACAAAATCTTCTTTTCGCCATGACATGAACCTCAGAAAAAC  
ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT

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FIGURE 2I

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTTCGTCCACATACTCTCTATGTACAT  
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT  
CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT  
CCAAATAACTGTAGTGGAGTAAGAAAGAGACGTCTGTCAAATGTATCTTTACCAGGACCC  
GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCCAGTGAAGAGTCA  
CATGTCCACCAGGAACCAAGTAAGAGAATTCTCTTGGAGTGGTCGCCCAATCTGGATG  
GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC  
CGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTCTTTCGCCAAGGAATG  
CAGTGTAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAAGTACCAAGAGAC  
TGCCTTGGAGAGGTTACTTTCAATGGAGAACCCTTCCAGTCTGGGAACAGATACAGATATA  
CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA  
GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG  
GAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGCAATAATATTCGCTA  
ATGAGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAATGGTGAAGGAA  
GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAGAGGCATTATTGGAGACTT  
GACAGCAAATGTCTAACATTATTTCAGAATGAATCTGGATCAAAGTATTATAAGGAAAT  
CCACTTTCAGAAATCTCCGCATATCTTACCACGAGATTTCAAAACATTTACAAGGC  
AGCAATCCACACTGTTTTGAAATCATTACTGATACTATGGTATACTTCGTTGGTGAGAAC  
AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA  
CAGAGCTGGGAAAAGCAATTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGT  
TGCACTTCTCCAGGGCAAGGGAAAGATCACAAAGATTTGTCTACAAGTATCTCTGTATCT  
AATTGTGAGATTGAGGAGATGTGGATATCAGTACTGTTTACCAGATCTTTCAGATGAG  
GTGCTTGGTTCAGGCCAGTTTGGCATCGTTTATGGAGGAAAACATAGAAAGACTGGGAGG  
GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC  
CGTAATGAAGTGGCTATTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT  
ATGTTTGAAACCCCAAGAGTCTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG  
GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC  
ACACAGATACTTGTGCTTTGAGGAATCTGCATTTTAAGAATATTGTGCACTGTGATTA  
AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCTCAGGTGAAGCTGTGTGAC  
TTTGGATTTGCACGCATCATTGGTGAAAAGTCATTTCAGGAGATCTGTGGTAGGAACCTCA  
GCATACTTAGCCCTGAAGTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG  
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCTTTTAATGAGGATGAA  
GATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA  
ATTTCTGGTGAAGCAATTGATCTGATAAACAATCTGCTTCAAGTGAAGATGAGAAAACGT  
TACAGTGTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC  
CTTAGAGAATTTGAAACTCGCATTGGAGAACGTTACATTACACATGAAAGTGTATGCT  
CGCTGGGAAATACATGCATACACATAACCTTGTATACCCAAAGCACTTCATTATGGCT  
CCTAATCCAGATGATATGGAAGAAGATCCTTAA

SEQ ID NO: 12\_PKNBETA\_H

ATGGAGGAGGGGGCGCCGCGGCAGCCTGGGCGGAGCCAGTGGCCCCCAGAGGATGAGAAG  
GAGGTGATCCGCGGGCCATCCAGAAAGAGCTGAAGATCAAGGAGGGGGTGGAGAACCTG  
CGGCGCGTGGCCACAGACCGCGGCCACTTGGGCCATGTGCAGCAGCTGCTGCGGTCTCTCC  
AACCGCGCCTGGAGCAGCTGCATGGCGAGCTGCGGGAGCTGCACGCCCGAATCCTGCTG  
CCCGGCCCTGGGCTGGCCAGCTGAGCCTGTGGCCTCAGGACCCCGCGCTGGGCAGAG  
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG  
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCCAAGGAGAGGAAG  
CTCCTTGCAGCTGCCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG  
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGAGCCAGGGCCTGAGCTACTGGCG  
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGCGCCAAGAAGCTG

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## FIGURE 2J

GTGAAACTGCTTAGTAGCCGGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCAGGCC  
CAGCTACAGGAGTCTCTCAGAACTGGACCTCCTGCGCCTGGCCTTGGAGCAGCTGCTG  
GAGCAACTGCCTCCTGCCACCCCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG  
GTGCCTGGATAACCCCGAGCCTTCAGGGACACCTGTGAAGCCACCGCCCTAACAGGGACA  
CTGCAGGTCCGCCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA  
GCGGCCGCACTGGCCAGCAGCCCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG  
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGT  
GTGGGGCAGACGGGCTGGGGGCAAGTGGCCGAACAGTCTTGGGACCAGACCTTTGTCATC  
CCACTGGAGCGAGCCCGTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA  
TGTGGCGTGGCCTTCTGAGACTTGAAGACTTCTTGGACAATGCCTGTACCAACTGTTC  
CTCAGCCTGGTACCGCAGGGACTGCTTTTGGCCAGGTGACCTTCTGCGATCCTGTCTC  
GAGAGGCGGCCCGGCTGCAGAGGCAGGAACGCATCTTCTCTAAACGCAGAGGCCAGGAC  
TTCCTGAGGCGTTTCGCAGATGAACCTCGGCATGGCGGCCTGGGGGCGCCTCGTCATGAAC  
CTGCTGCCCCCTGCAGCTCCCCGAGCACAATCAGCCCCCTAAAGGATGCCCTCGGACC  
CCAACAACACTGCGAGAGGCCTCTGACCCTGCCACTCCAGTAATTTCTGCCCCAGAAG  
ACCCCTTGGGTGAAGAGATGACACCCCCACCAAGCCCCACGCCTCTACCTCCCCAG  
GAGCCAACATCCGAGGAGACTCCGCGCACCAACAGTCCCCATATGGAGCCTAGGACTCGA  
CGTGGGCCATCTCCACCAGCCTCCCCACCAAGAAACCCCTCGGCTTCAGGACTTCGCG  
TGCTTAGCTGTGCTGGGCCGGGACACTTTGGGAAGGTCTCCTGGTCCAGTTCAAGGGG  
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGACGAG  
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCT  
TTCTGCTCTCCCTCCTTGTCTGCTTCCAGACCTCCAGCCATGCCCGCTTTGTGACTGAG  
TTTGTGCTGCTGGTGGTGAACCTCATGATGCAGATCCACGAGGATGTCTTCCCCGAGCCCCAG  
GCCCCCTTCTACGTGGCTTGTGTTGCTCCTGGGCTGCAGTTCTTACACGAGAAGAAGATC  
ATTTACAGGGACCTGAAGTTGGATAACCTTCTGCTGGATGCCAGGGATTCTGAAGATC  
GCAGACTTTGGACTCTGCAAGGAAGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT  
GGCACCCCGAGTTCTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACAGGCCGTC  
GACTGGTGGGCGCTGGGTGTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCA  
GGGGACACAGAGGAAGAGGTGTTTGAAGTGCATCGTCAACATGGACGCCCCCTACCCGGC  
TTTCTGTGCGTGCAAGGGCTTGAGTTTATTGAGAGCTCCTCCAGAAGTGCCCGGAGAAG  
CGCCTCGGGGAGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC  
ACCAACTGGCAAGCCCTGCTCGCCCGACCATCCAGCCCCCTTCGTGCCTACCCTGTGT  
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACC  
CCACCTGCACCCACAGCCTCCTCACTGCCCGCCAACAGGCCGCTTCGGGACTTCGAC  
TTTGTGTGAGAGCGATTCTTGAACCTGA

SEQ ID NO: 13\_AI021023\_M PKNBETA\_M  
GCTGAAGTGGGATAACCTTCTGCTGGATGCCAGGGATTCTGAAGATCGCAGACTTTGG  
ACTCTGCAAGGAAGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGTGGCACCCCGGA  
GTTCTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACAGGGCTGTGGACTGGTGGG  
GCTGGGTGTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCAGGGGACACAGA  
GGAAGAGGTGTTTGAAGTGCATCGTCAACATGGACGCCCCCTACCCGGCTTTCTGTGCT  
GCAAGGGCTTGAGTTTATTGAGAGCTCCTCCAGAAGTGCCCGGAGAAGCGCCTCGGGG  
GGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACCACCAACTGGCA  
AGCCCTGCTCGCCCGACCATCCAGCCCCCTTTGTGCTTACCCTGTGTGGCCCTGCGGA  
CCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACCCACCTGCACC  
CCACAGCCTCCTCACTGCCCGCCAACAGGCCGCTTCGGGACTTCGACTTTGTGTGAGT  
GCGATTCTTGAACCTGAGGGCATCTCCTGGCACCTCTGTCCCCTTCCCCACAGACTG  
TTAGAGCCTCTGCTCGTTACCCGTCGCTGGAGGTCCAGGCCTTGTGGGTAC  
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGCTCAG

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## FIGURE 2K

TGTCACTGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA  
GACCTGGCCCAGAAAGGGTGCCGCAGCAAGGAGTGATATGGTTTGTCTTTTAAAGACTGG  
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14\_H19102\_H

GGTGGCAACATCCGGGGTCCCTGGGCCCCGAGGCTGGAAGAGCCTCTGGACAGGTTTGGGA  
ACCATCAGGTCAGATCTGGAAGAACTCTGGGAACCTACGGGGGCACCACTATCTGCACCAG  
GAATCCCTAAAGCCAGCCCCAGTACTGGTAGAGAAGCCTCTGCCAGAGTGGCCAGTGCCT  
CAGTTCATCAACCTCTTTCTACCAGAGTTTCCCATTAGGCCCATTAGGGGGCAGCAGCAG  
CTGAAGATTTTAGGCCTCGTGGCTAAAGGCTCCTTTGGAAGTGTCTCAAGGTGCTAGAT  
TGCACCCAGAAAGCTGTATTTGCAGTGAAGGTGGTGCCCAAGGTAAAGGTCTTACAGAGG  
GATACCGTGAGGCAGTGCAAAGAGGAGGTAGCATCCAGCGACAGATCAACCATCCCTTT  
GTACACAGCTTGGGGGACAGCTGGCAGGGAAAACGGCACCTTTTTCATTATGTGTAGCTAC  
TGCAGCACAGATCTGTACTCCCTTTGGTCTGGCTGTTGGCTGCTTTCCCTGAGGCTTCCATC  
CGTCTCTTTGCTGCCGAGTTGGTGTCTGGTACTGTGTTATCTCCATGACTTGGGCATCATG  
CATCGAGATGTGAAGATGGAGAATATTCTTAGATGAACGAGGCCATCTGAACTGACA  
GACTTTGGTCTGTCCCGCCACGTGCCCCAGGGAGCTCAAGCCTACACTATCTGTGGCACT  
CTTCAGTACATGGCCCCAGAGTCTTAAGTGGAGGACCTTACAACCATGCTGCTGATTGG  
TGGTCCCTGGGTGTCTTGCTTTTCTCTCTGCGACTGGAAAGTTTCCAGTGGCTGCAGAG  
AGAGATCATGTGGCCATGTTGGCAAGTGTGACCCACAGTGAAGTCTGAGATCCCAGCTTCT  
CTTAACCAGGGCCTCTCACTCCTGCTCCATGAGCTCTTATGCCAGAACCCCTCCATCGT  
CTACGTTATCTGCATCACTTCCAGGTCCACCCTTTCTTTGCGGGTGTGGCCTTCGACCCA  
GAGCTCCTACAGAAGCAGCCAGTGAAGTTTGTACGGAGACACAAGCTACCCAGCCAGT  
TCAGCGGAGACCATGCCCTTTGACGACTTTGACTGTGATCTGGAGTCCTTCTTGCTCTAC  
CCTATCCCTGCTTGA

SEQ ID NO: 15\_AA476563\_H

ATGGAATTCTTTAGGATAGACAGTAAGGATAGCGCAAGTGAAGTCTTGGGACTTGACTTT  
GGAGAAAAATGTATAGTCTAAAATCAGAACCTTTGAAACCATCTTTACTCTTCCAGAT  
GGAGACAGTGTCTTAGGAGTTTTAATACTAGTGAAGCAAGGTAGAGTTTAAAGCTCAG  
GACACCATTAGCAGGGGCTCAGATGACTCAGTGCCAGTTATTTGTTTTAAAGATGCTGCT  
TTTGATGATGTGAGTGTACTGATGAAGGAAGACCTGATCTTCTTGTAATTTACCTGGT  
GAATTGGAGTCAACAAGAGAAGCTGCAGCAATGGGACCTACTAAGTTTACACAACTAAT  
ATAGGGATAATAGAAAATAAACTCTTGGAAAGCCCTGATGTTTATGCCTCAGGCTTAGT  
ACTGAACAATGCCAAGCACATGAGGAGAAAGGCATAGAGGAAGTGAAGTATCCCTCTGGG  
CCCAAATCCTATAGTATAACAGAGAAACACTATGCACAGGAGGATCCCAGGATGTTATTT  
GTAGCAGCTGTTGATCATAGTAGTTTCAAGGAGATATGTCTTTGTTACCCAGCTCAGATCCT  
AAGTTTCAAGGACTTGGAGTGGTTGAGTCAGCAGTAACTGCAAAACAACAGAGAAAGC  
TTATTCCTGATTTGTAGTCCACTCTCAGGTGCTAATGAATATATTGCAAGCACAGACACT  
TTAAAAACAGAAGAAGTATTGCTGTTTACAGATCAGACTGATGATTTGGCTAAAGAGGAA  
CCAATTCTTTATTCAGAGAGACTCTGAGACTAAGGGTGAAAGTGGTTTAGTGCTAGAA  
GGAGACAAGGAAATACATCAGATTTTGGAGACCTTGATAAAAAATTAGCACTAGCCTCC  
AGGTTTTACATCCCAGAGGGGCTGCATTCAAAGATGGGCAGCTGAAATGGTGGTAGCCCTT  
GATGCTTTACATAGAGAGGGGAATTGTGTGCCGCGATTGTAACCCAAACAACATCTTATTG  
AATGATAGAGGACACATTCAAGTATTTTAGCAGGTGGAGTGAGGTTGAAGATTCC  
TGTGACAGCGATGCCATAGAGAGAAATGTACTGTGCCCCAGAGGTGGAGCAATCACTGAA  
GAACTGAAGCCTGTGATTGGTGGAGTTGGGTGCTGTCTCTTTGAACCTCTCACTGGC  
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA  
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATTCAACAGCTCTTGCAAGTTCAATCCTCTG

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## FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTGAAGATATCAAATCTCATCCATTTTACC  
CCTGTGGATTGGGCAGAACTGATGAGATGA

SEQ ID NO: 16\_AA626690\_H  
ATGCTACCATTGCTCCTCAGGACGAGCCCTGGGACCGAGAAATGGAAGTGTTACGCGG  
GGCGGCGGAGCAGCGGCGAGGTAAATGGTCTTAAATGGTTGATGAGCCAATGGAAGAG  
GGAGAAGCAGATTCTTGTCATGATGAAGGAGTTGTTAAAGAAATCCCTATTACTCATCAT  
GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTG  
CAGGGGTCATTTGGAAAGGTTTTCTTGTTAGAAAGAACCGGTCCTGATGCTGGGCAG  
CTCTATGCAATGAAGGTGTTAAAAAAGCCTCTTAAAGTTTCGAGACAGAGTTCGGACA  
AAGATGGAGAGGGATATACTGGTGGAAGTAAATCATCCATTTATTGTCAAATTGCACTAT  
GCCTTTCAGACTGAAGGGAAGCTGTACTTAATACTGGATTTTCTCAGGGGAGGAGATGTT  
TTCACAAGATTATCCAAAGAGGTTCTGTTTACAGAGGAAGATGTGAAATTCTACCTCGCA  
GAACTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG  
CCAGAAAACATTTTGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGACTCAGC  
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTTGTTACAGTAGAGTATG  
GCTCCTGAAGTAGTAAATAGGAGAGGCCATTCCCAGAGTGCTGATTGGTGGTCATATGGT  
GTTCTTATGTTTGAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG  
ACCATGAATATGATATTAAAGCAAACTTGGAAATGCCTCAATTTCTTAGTGCTGAAGCA  
CAAAGTCTTCTAAGGATGTTATTCAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA  
GTTGAAGAAATCAAAGACATCTGTTTTTTGCAAATATTGACTGGGATAAATTATATAAA  
AGAGAAGTTCAACCTCCTTCAAACCTGCTTCTGGAAAACAGATGATACTTTTGTGTTT  
GATCCTGAATTTACTGCAAAAACACCTAAAGATTCTCCCGGTTTGCCAGCCAGTGCAAT  
GCTCATCAGCTCTTCAAAGGATTGAGCTTTGTTGCAACTTCTATTGCAGAAGATATAAA  
ATCACTCCTATCACAAGTGCAATGTATTACCAATTGTTGAGATAAATGGAATGCTGCA  
CAATTTGGTGAAGTATATGAATTGAAGGAGGATATTGGTGTGGCTCCTACTCTGTTG  
AAGCGATGCATACATGCAACTACCAACATGGAATTTGCAAGTGAAGATCATTGACAAAAGT  
AAGCGAGACCCTTCAAGAGAGATTGAAATATTGATGCGCTATGGACAACATCCCAACATT  
ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTAAATG  
AAAGGAGGAGAGTTACTTGACCGTATTCTCAAACAAAATGTTTCTCGGAACGGGAGGCT  
AGTGATATACTATATGTAATAAGTAAGACAGTTGACTATCTTCATTGTCAAGGAGTTGTT  
CATCGTGATCTTAAACCTAGTAATATTTTATACATGGATGAATCAGCCAGTGCAGATTCA  
ATCAGGATATGTGATTTTGGGTTTGCAAAACAACTTCGAGGAGAAAATGGACTTCTCTTA  
ACTCCATGCTACACTGCAAACTTTGTTGCACTGAGGTTCTTATGCAACAGGGATATGAT  
GCTGCTTGATATCTGGAGTTTAGGAGTCTCTTTTACACAATGTTGGCTGGCTACACT  
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA  
AAATTCTCTTTGAGTGGTGGAACTGGGACAATATTTGAGACGGAGCAAAGGATTGCTT  
TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAGCAC  
TCATGGATAACTCAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA  
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTTCAA  
CCAGTCCCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCAGCGAGCGAGCATGAAAAGCGA  
ACATCAACTGGCCTGTAA

SEQ ID NO: 17\_AA215680\_H  
ATGAGCCTGGTGGCCTGTGAGTGCCTGCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA  
CGAGCACGGTCCCAAGCTCACGTGTACCTGGAGCAGATTTCGCAACAGGGTGGCTCTGGGA  
GTGCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC  
CTGGAGCGCGATGTTAGTGAGGACTATGAGGCGGCCCTTCAACCACTATCAGAATGGCGTG  
GACGTGCTGCTCCGTGGCATAACGTTGACCCCAACAGGAGCGAGCTGAGGCTGTGAAG  
CTGAAAATTACCAATACCTGCGGCGGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

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## FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGGGTTTCAGCAGCCTGAGGCTCCGGCCCAT  
 CGCACGCTGAGCTCTGCCGTGGAGCAGCTGAGGGCTGCAGGGTGGTCGGGGTCATCGAG  
 AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC  
 AGGTGCCACATGGTGAGCAGGGAGCGGCTGACCATCATCCACACGAGTCCCCTACATG  
 ACGAAGCTGCTCAGGTACTTTGTGAGCGAGGACTCCATCTTCTGACACCTGGAGCATGTG  
 CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCAGGCGCACTCCCGACATTCTGGGCTC  
 AGCTCTGGCTCTACCCAGGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG  
 ACCCCAGCGAGGCTTCCCTCAGGCCATGCCCTGGCCAGGACAGAATCGCCCTGGAGCCT  
 CCTAGGACTTCTCCGAACCTTCTCCTAGCTGGGGAGGCCCCATCCACAGACCCCAGAGG  
 GAGGCTGAAGGTGAACCCACAGCCAGGACCAGCACCTCTGGCTCCTCGGACCTTCCAAAG  
 GCCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAACTCAGACGCTGGG  
 CCCCCTCGGGGGCTCACTTGGGTTCTGAGGGGGCGGGCCGGTGTAGGGGGCTGTGGC  
 CGAGGCATGGATCAGAGCTGCCTGTCAGCAGATGGGGCCGGCCGGGCTGTGGCAGGGCC  
 ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG  
 GAGGCGCTGCACGAGCAGGGGTGCTGTGCCGGGACCTCCACCCGGGAACCTGCTCCTG  
 GACCAGGCAGGTACATCCGGCTCACATATTTTGGCCAGTGGTCAGAGGTGGAGCCCCAG  
 TGCTGCGGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGTGGGATTTCAGG  
 CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAACTGCTGACGGGA  
 ATGGCACTGTCCCAGAGCCACCTTCAGGAATCCAGGCCCCACCCAGCTCCAGCTGCCC  
 GAGTGGCTCAGTCGCCCAGCGGCTCTCTGCTGACTGAGCTGCTGCAGTTTCAGCCTACC  
 CGGCGCTGGGCATGGGAGAAGGTGGTGTGAGCAAACTCAAGTCCCATCCCTTTTTAGT  
 ACCATCCAATGGAGCAAGCTGGTGGGTAA

SEQ ID NO: 18\_SGK\_H  
 ATGACGGTGAAAACTGAGGCTGCTAAGGGCACCTCACTTACTCCAGGATGAGGGGCATG  
 GTGGCAATTCTCATCGCTTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTAG  
 AAGATTGCCAATAACTCCTATGCATGCAACACCCTGAAGTTCAGTCCATCTTGAAGATC  
 TCCCAACCTCAGGAGCCTGAGCTTATGAATGCCAACCTTCTCCTCCACCAAGTCTTCT  
 CAGCAAATCAACCTTGGCCCGTCGTCCAATCCTCATGTAAACCATCTGACTTTCACTTC  
 TTGAAAGTGATCGGAAAGGGCAGTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGAGGAG  
 GAAGTGTCTATGCAGTCAAAGTTTTACAGAAGAAAGCAATCCTGAAAAAGAAAGAGGAG  
 AAGCATATTATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCTTTCTGGTG  
 GGCCTTCACTTCTCTTCCAGACTGCTGACAAATTGTACTTTGTCTTAGACTACATTAAT  
 TTTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCTGCATTCACTGAACATCGTTTAT  
 AGAGACTTAAACAGAGAATATTTTGCTAGATTACAGGGACACATTGTCTTACTGAT  
 TTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACAACTCCACCTTCTGTGGCAGG  
 CCGGAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAGGACTGTGGACTGG  
 TGGTGCCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCCGCTTTTATAGCCGA  
 AACACAGCTGAAATGTACGACAACATTCTGAACAAGCCTCTCCAGCTGAAACCAAATATT  
 ACAAATTCCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAAGGACAGGACAAAGCGGCTC  
 GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTTAATTAAGTGG  
 GAGTACGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCAAACTCCATTGGCAAG  
 TCCCCTGACAGCGTCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCCTAGGC  
 TTTTCTATGCGCCTCCACGGACTCTTTCCTCTGA

SEQ ID NO: 19\_AA107515\_M  
 CGGGTCCGACCCACGCGTCCGCCGGTTTCACTGCTCCCCCTCAGTCTCTTTTGGGCTCTTTC  
 CGGGCATCGGGACGATGACCGTCAAAGCCGAGGCTGCTCGAAGCACCTTACCTACTCCA



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## FIGURE 20

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTTGA  
CCCAGAGTTCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC  
CAGCAGCTCTGGGGCCTCAAGTGCATTCTTGGGATTTTCTTATGCGCCAGAGGATGATGA  
CATCTTGGATTGCTAGAGAGAAGGACCTGTGAACTACTGAGGCCAGCTGGTATTAGTA  
AGGAATTACCTTCAGCTGCTAGGAAGAGCGACTCAAATAACAATGGCTTCAACGAGAAG  
CAGGTTTATTTTTTCCAGCACATAAAAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAG  
GACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTT  
CCAATGTTAGGTTTGCTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTAG  
GGAAGGGAAAATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCA  
AAGCTCCACCCAATGACTTCTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG  
AGGCTGGGAGATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGGTTT  
TGACACTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCACTCTTTTACCAGAGGG  
CCTCCTGGTGTGTTGATTTTGTATCTCAATGTGTAAAATGACAGAGATGTAACAAGCTCAT  
AGGGTATCAATATCTCTTATTGTTCT

SEQ ID NO: 21\_AA887783\_H  
CGGATGCATTINTTGGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACT  
ACAAGGAAAGCTGCCCAAGTGTAAGNATTCAGCTCCGATGAACACAGAGAGAAAAAGA  
AGAGGTTTACTGTTTATAAAGTTCTGGTTTCAGTGGGAAGAAGTGAATGGTTTGTCTTCA  
GGAGATATGCAGAGTTTGATAAACTTTATAACTTTAAAAAACAGTTTCTGCTANGG  
CCCTGAAGATTCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAC  
AAAGACGAGCAGGACTAAACGAATTCATTGAGACCTAGTTAGGTATCCAGAACTTTATA  
ACCATCCAGATGTGAGAGCATTCTTCAAATGGACAGTCCAAAACACCACTCAGATCCAT  
CTGAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCAGAAATCAACC  
TGGGACCGTCTGGAAATCCTCATGCCAAACCACTGACTTTGATTTCTTAAAGTTATTG  
GAAAAGGCAGCTTTGGCAAGGTTCTTCTTGCAAAACGGAACCTGGATGGAAAATTTATG  
CTGTCAAAGTGTTACAGAAAAAATAGTTCTCAACAGAAAAGAGCAAAAACATATTATG  
CCTTCCAAACAAGCTTTATTTGTTCTGGAATTTGTTAATGGAGGGGAGGGAC  
ATGTTGTCTTAACAGATTTTGGGCTTTGTAAAGAAGGAATTGCTATTTCTGACACCACTA  
CCACATTTTGTGGGACACCAGAGTATCTTGACCTGAAGTAATTAGAAAACAGCCCTATG  
ACAATACTGTAGATTGGTGGTGCCTTGGGGCTGTTCTGTATGAAATGCTGTATGGATTG  
CTCCTTTTTTATTGCCGAGATGTTGCTGAAATGTATGACAATATCCTTCACAAACCCCTAA  
GTTTGAGGCCAGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAACTCCTAGAAAAAG  
ACAGGCCAAAATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAAATCATCCTTTT  
TTGAATCACTCAGCTGGGCTGACCTTGTAACAAAAGAAAGATTCCACCACCATTTAATCCTA  
ATGTGGCTGGACCAGATGATATCAGAACTTTGACACAGCATTTACAGAAGAAACAGTTC  
CATATTCTGTGTGTGTATCTTCTGACTATTCTATAGTGAATGCCAGTGTATTGGAGGCAG  
ATGATGCATTGCTTGGTTTCTCTTATGCACCTCCTTCAGAAGACTTATTTTGTGAGCAG  
TTTGCCATTGAGAAACCATTTGAGCAAAATAAGTCTATAGATGGGACTGAACTTCTATTT  
GTGTGAATATATTCAAATATGTATAACTAGTGCCTCATTTTATATGTAATGATGAAAAC  
TATGAAAAATGTATTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCTGTTT  
TGATTAATAATTTATATTCTTGTGTTAATAAGCTTATTTTAAACAATTTAAAGCTATTAT  
TCTTAGCATTAACCTATTTTTTAAAGAAACCTTTTTTGCTATTGACTGTTTTTCCCTCTA  
AGTTTACACTAACATCTACCCAAGATAGACTGTTTTTAAACAGTCAATTCAGTTCAGCT  
AACATATATTAATACCTTTGTAACCTTTGCTATGGCTTTTGTATCACACCAAACTAT  
GCAATTGGTACATGGTTGTTAAGAAGAAACCGTATTTTTCATGATAAATCACTGTTTG  
AAATATTTGGTTTATGGTATGATCGAAATGTAAAAGCATAATTAACACATTGGCTGCTAG  
TTAACAATTGGAATAACTTTATCTGCAGATCATTTAAGAAGTAACAGGCCGGCGCGGT  
GGCTCACGCTGTAATCCAGCACTTTGGGAGGCTGAGGCCGGCAGATCACCTGAGGTCA

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FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAAT  
 TGGCAGGGTGTGGTGGCACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGA  
 ATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACTCCTG  
 CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22\_R47805\_H

ATGGCGCACCAAACGGGCATCCACGCCACGGAAGAGCTGAAGGAATTCTTTGCCAAGGCA  
 CGGGCTGGCTCTGTGCGGCTCATCAAGGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGT  
 GCCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGCTGCTGCCACTG  
 CTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCCTCGACTCACAGAATGCTCAGGGC  
 TTCGAATGGCTCTTCTCGCCTGGTTCGCTGATAACTCCCCCGTGCGGCTGAAGATGCTG  
 TACGCGGCCACGCGGGCCACAGTGAAGGAGGTTTGGAGGTGGCCACATCAAGGATGAG  
 CTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGGCTGGGTACCAGAAACACCTGTCGTCC  
 TGTGCGGCACCTGCCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAAC  
 GAGGTGAAGACAGAGATCAGTGTGGAAGCAAGCACCAGACCCTGCAGGGCCTCGCCTTC  
 CCCCTGCAGCCTGAGGCCAGCGGGCACTCCAGCAGCTCAAGCAGAAAATGGTCAACTAC  
 ATCCAGATGAAGCTGGACCTAGAGCGGGAAACCATTGAGCTGGTGCACACAGAGCCACG  
 GATGTGGCCAGCTGCCCTCCCGGGTGCCTCCGAGATGCTGCCCGCTACCACTTCTTCTC  
 TACAAGCACACCCATGAGGGCGACCCCTTGAGTCTGTAGTGTTCATCTACTCCATGCCG  
 GGTACAAGTGCAGCATCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCTCCTC  
 GACTCCGTGGAGCAGGACTTCCATCTGGAGATCGCCAAGAAAATTGAGATTGGCGATGGG  
 GCAGAGCTGACGGCAGAGTTCTCTACGACGAGGTGCACCCCAAGCAACACGCCTTCAAG  
 CAGGCCTTCGCCAAGCCCAAGGGCCAGGGGGCAAGCGGGGCCATAAGCGCCTCATCCG  
 GGCCCGGGTGAAAATGGGGATGACAGCTAG

SEQ ID NO: 23\_H60215\_H

CCACGCGTCCGGCGCCCGCAGCCATGGAGGGAGGCGGCGGCGGCGGCGGCGGCTCGGG  
 TGGCTGCGCTGGGAGGCGGCGGTGAGAGGCTCGCACGCCTCCAGCCCCGGCCCCCGCCCC  
 CGGGAGGGAGAGCCGAGCAGCCCCGGCTCTGGGCTACGGACTATGGGCGAATAGCTCTGA  
 CCACCCGGCGAAGTGACACACCCAGAAGCTATGTCCTTCGGCAGTAAAAGTTTTACAGC  
 ACAATATATGTGCTCTGCTCTCTCCCGCAATCCTGCTCCAAGAGATCTTAAGCTGGAGG  
 CACCAGGTCTGAATTCAGACTCCTCCCCACCACCCACACTTCACCTCCAAGTGGAGCAT  
 GACCACAGACCCATTGAGGGAGGCTGGCGGACTCTTCATCCTGGACAGTCCCTTACTGTA  
 TGTCAAAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCGGCCA  
 GGGCCAAGGCTCTAGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTCA  
 TCCTTGGTCCCCGTCTGGGCAACTCACCGGTGCCAAGCATAGTGCAGTGTGTCGGAGGA  
 AAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCTGGAGGAGAGGGGGGACC  
 AAGGCATAGAGAGCCAGGAAGAGCGGCAAGATGCTGCTGCACACCGAGTACTCAC  
 TGCTGTCTCTCTGCAACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACC  
 GCACCTGTGAAATCGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGC  
 GCATCTGCCTCGTCTGGACTGCCTCTGTGCTCATGACTTCAGCGATAAGACCGCTGACC  
 TCATCAACCTGCAGCACTACGTATCAAGGAGAAGAGGCTCAGCGAGAGGGAGACTGTGG  
 TAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAATATCGTGCACA  
 GAGACCTGAAGCTGGGGAACATGGTGTCTCAACAAGAGGACACATCGGATAACCATCACCA  
 ACTTCTGCCTCGGGAAGCATCTGGTGGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGA  
 GCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCGCGGTACCGTGGCAAGCCAGTG  
 ACATGTGGGCCCTGGGCGTGGTGTCTTCCACATGCTGTATGGCCAGTTCCCCTTCTACG  
 ACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATAACATTCTGAGG  
 ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTGACCCCC  
 AGCAGCGCCTGGCCCGCCGACGTCTGGAGGCCCTCAGTGCCATCATTGCATCATGGC

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## FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTGCAAGTGGTTCCTGACATTGATGACCAAATGA  
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCAGTACGAGTTTG  
AGAACTACATGCGTCAGCAGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACACCC  
GGAGCTGGGTACCCAAGCGGCAGTTCGGCAGCGCACCAACCGGTGCGACGGCTGGGCCACG  
ACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCTACCTGCGGAAAT  
AACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCG  
TGGCTGTGAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGC  
AGGGACAGGGACAGCCAGGTACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTT  
TGGGATGATTGCTCGATTGTTTGGTTTTTAATCTGAGAAGCCTAGATAACTAATCTGCT  
TTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTCTCTGGACTGAGC  
AAGAGGGAGGAGGGAGCCTGCTCACCCTACTCCAGGGCCTTCCCCAGCGGCCACCACTG  
ACCTGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGACGCTCGCTGCAGGCCCC  
AGAGCGAGCTTCCCCCTCCTCCCTGCTCTCCAGGGCCCTGCCACAGCCTCTTTCCGTCCC  
TCTCTTTCTGATCCAGGCCCCCTCAGTCCAAGCTTTGGAAAACCTTCACCTCATCTTAAAC  
CAAACCTCAAATATATTTATTTTTTTTACCAT

SEQ ID NO: 24\_SGK324\_H  
GCCGCGATGGCCAGCACCAGGAGTATCGAGCTGGAGCACTTTGAGGAACGGGACAAAAG  
CCGCGGCCGGGGTTCGCGGAGAGGGGCCCCAGCTCCTCCGGGGGCAGCAGCTCGGGC  
CCCAAGGGGAACGGGCTCATCCCCAGTCCGGCGCACAGTGCCCACTGCAGCTTCTACCGC  
ACGCGGAACCTGCAGGCCCTCAGCTCGGAGAAGAAGGCCAAGAAGGCGCGCTTCTACCGG  
AACGGGGACCGCTACTTCAAGGGCCTGGTGTGTTGCCATCTCCAGCGACCGCTTCCGGTCC  
TTCGATGCGCTCCTCATAGAGCTCACCCTGCTCCCTGTGCGACAACGTGAACCTGCCCCAG  
GGTGTCCGCACTATCTACACCATCGACGGCAGCCGGAAGGTACACGCTGGACGAGCTG  
CTGGAAGGTGAGAGTTACGTGTGTGCATCCAATGAACCATTTTCGTAAAGTCGATTACACC  
AAAAATATTAATCCAACTGGTCTGTGAACATCAAGGGTGGGACATCCCGAGCGCTGGCT  
GCTGCCTCCTCTGTGAAAAGTGAAGTAAAAGAAAGTAAAGATTTTCATCAACCCCAAGTTA  
GTGACTGTGATTGAAAGTGGAGTGAAGCCTAGAAAAGCCGTGCGGATCCTTCTGAATAAA  
AAGACTGCTCATTCTTTGAACAAGTCTTAACAGATATCACCGAAGCCATTAAACNAGCC  
TCAGGAGTCGTCAAGAGGCTCTGCACCCTGGATGGAAAGCAGGTGAGAGTTACGTGTGTG  
CATCTGCCAGACTTTTTTTGGTGATGACGATGTTTTTATGTCATGTGGACCAGAAAAATTT  
CGTTATGCCCCAAGATGACTTTGTCTGGATCATAGTGAATGTGCTGTCTGAAGTCATCT  
TATTCTCGATCCTCAGCTGTAAAGTATTCTGGATCCAAAAGCCCTGGGCCCTCTCGACGC  
AGCCAGATTTCTGCTCATGGCAGATCTTCTTCCAATGTAAACGGTGGACCTGAGCTTGAC  
CGTTGCATAAGTCCTGAAGGTGTGAATGGAAACAGATGCTCTGAATCATCAACTCTTCTT  
GAGAAATACAAAATTGGAAAGGTCAATTGGTGATGGCAATTTTGCAAGTAGTCAAAGAGTGT  
ATAGACAGGTCCACTGGAAAGGAGTTTGCCCTAAAGATTATAGACAAAGCCAAATGTTGT  
GGAAAGGAACACCTGATTGAGAATGAAGTGTCAATACTGCGCCGAGTGAAACATCCCAAT  
ATCATTATGCTGGTCGAGGAGATGGAAACAGCAACTGAGCTCTTTCTGGTGATGGAATTG  
GTCAAAGGTGGAGATCTCTTTGATGCAATTACTTCGTGACCAAGTACACTGAGAGAGAT  
GGCAGTGCCATGGTGTACAACCTTAGCCAATGCCCTCAGGTATCTCCATGGCCTCAGCATC  
GTGCACAGAGACATCAAACCAGAGAATCTCTTGGTGTGTGAATATCCTGATGGAACCAAG  
TCTTTGAAACTGGGAGACTTTGGGCTTGCGACTGTGGTAGAAGGCCCTTTATACACAGTC  
TGTGGCACACCCACTTATGTGGCTCCARAAATCATTGCTGAAACTGGCTATGGCCTGAAG  
GTGGACATTTGGGCAGCTGGTGTGATCACATACATACTTCTGTGGATTCCCACCATTC  
CGAAGTGAGAACATCTCCAGGAAGATCTTTCGACCAGATCTTGGCTGGGAAGCTGGAG  
TTTCCGGCCCCCTACTGGGATAACATACGGACTCTGCCAAGGAATTAATCAGTCAAATG  
CTTCAGGTAAATGTTGAAGCTCGGTGTACCGCGGGACAAATCCTGAGTCACCCCTGGGTG  
TCAGATGATGCCTCCAGGAGAATAACATGCAAGCTGAGGTGACAGGTAAACTAAAAACAG  
CACTTTAATAATGCGCTCCCCAACAGAACAGCACTACCACCGGGGTCTCCGTTCATCATG

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## FIGURE 2R

GTGAGTGGAAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA  
 GGTAGCCGGGAGCTGCCCTCACATGGAAGTTGGTGCCTTCCGTAGTCCTATTTTCATATGA  
 AGATTGGCTTGGCATGTGGAGGGCACTCATTCGGCAACTCCCAGGCTTTGGGCACTGTGT  
 GGAGGGGCTTGTGTAGGGACCAGAGGCCTGGTGTGAGGGGTCCAGGCGTCAAGGAGCTC  
 CTGGCTGGGCCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA  
 CTCCCCAAGCCCTGGAGGGGTGTGTTGTGTTAGGAATTAACCTCCCTGCCTACCCCAAGGCC  
 TCAGAAATAGATTATTAGAGATGTGAATTATTCTTTGAGACTTGGGATAAGAAACAGCCA  
 AAGCTAAACATATTTTCAGTTTTTAAAAAATCAGTGTTTTATAAAACACAGTTTGGGGCTTT  
 TAAAGGTACATAATCAAGGAAAAAATATATTTTTCAGGCTTTTCTTCTTCCAAAATGTT  
 TGAGATGTCAGTGACAACGATGGCCTTATTTTTTTCAGCCTTTTCTTCTTCCAAAATGTT  
 TCTTAAGGCAACTCTCCTAAATACATAAAACACAACAAATTAATGAAGAGTGACATGAG  
 AGTAAATGAATCAAAAGGAAAAAACATTGAACCCAGAGGTGAGGGCAGCACACCCGCAGCA  
 GCTGTCCAGGCCTGAGCCAATGCAACCCCTGGGCGGGAAGGCCAGCTCACCGTGAGCAGGT  
 AGAAGCCAGCCAGCCACCCAGGCAGGGACCTTGGTTCTCCCCACACACTCCCAGGAGCAG  
 GGAACAGGGGTGGAGTGGCCTTTCCAGAGCTGGAGTTGGCTGCAGCAGCTTTCGAATCA  
 GACCTGCCAAGGTGATGGGCGTCTGAGTTTTCATCTGGGCCCCCGTGACCCCACTGAG  
 TCCTGACAGCTAAGGATGGGCCACCTCCACAGCTCCGTCCTGCTACTTGGGACAGGCCT  
 CTCATCCTCTGGGAAGGTCTCCTTGTCTTCTACCCAACTAGAAGGGAAACAGTGGCATA  
 TTCTCATGGTACATGGTTGTCTGAAAGCCTTACCTAGGAAGACGCAGGGTCTAGATAGAA  
 GCTATAAGGAAGCCACACACATAACCCACATCCCCACACCCCAACATCCCCCACTCC  
 CCACACCCCCCACACCCCCACATCCCCACCATAATTACCCCCACCTCCAAATATCTCAT

SEQ ID NO: 25\_W30246\_M SGK324\_M

ACCAAGTCCTCCAGCTCCTCTCCAACCAGCCCGGGAAGTTTCAGAGGATTGAAGATTTCT  
 GCTCAGGGCAGATCTTCTTCCAACGTAAACGGTGGGCTGAACCTGACCGTTGCCTGAGC  
 CCTGAAGGTGTGAATGGAAACCGGTGCTCCGAGTCGTTCCCCCTTCTGGAGAAATACAGA  
 ATAGGGAAGGTTCATCGGGGACGGCAACTTCGCGGTAGTTAAGGAGTGCCTGGACAGGTAC  
 ACTGGAAGAGATTGTCATTAAAGATTATAGACAAAGCCAAATGCTGTGGAAAGGAGCAT  
 CTGATTGAGAACGAAGTGTCAATCCTGCGCCGAGTGAAGCACCCCAACATCATCATGTTG  
 GTTGAAGAGATGGAAACAGCAACTGACCTCTTCTAGTGATGGAACTGGTCAAAGGTGGA  
 GATCTCTTTGATGCGATTACCTCTTCAACCAAGTACACTGAGAGAGATGGAAGCGCCATG  
 GTGTACAACCTAGCCAATGCCCTCCGGTACCTGCACAGCCTCAGCATCGTCCACAGGGAC  
 ATCAAGCCTGAGAATCTGCTGGTGTGCGAATACCCAGATGGAACCAAGTCTTTGAAGCTG  
 GGAGACTTTGGGCTGGCGACGGTGGTTGAAGGCCCGTTGTACACGGTCTGTGGCAGGCCA  
 ACTTATGTGGCACCAGAGATCATAGCTGAAACAGGTTATGGCCTGAAGGTGGATGTTTGG  
 GCAGCTGGTGTGATTACATACATACTCTCTGTGGATTCCCACCATTCCGGAGTGAGAAC  
 AATCTCCAGGAAGATCTCTTTGACCAGATCTTGGCTGGAAAGCTGGAATCCCAGCCCCC  
 TACTGGGACAACATTACAGACTCTCCTTGTGTGTGTTTTAGGAAATGCTTATGAAGCTGG  
 CCCGTGGGCTTCCCAGTGGGACGTGCAGCAGTTCTTGGCAGAGCAGGGCCAGCTCTGCTG  
 TGTCACTCCAGGGTCTCCCATCACCTCTGCTCTTTGCCATGGCAGGTCTGCTGAGACCC  
 CGCGGGGACGGGGGATGGTGTCTCCCTGATTGGCCTGTGACCAACCTTCTGGAAGGCTGC  
 TGGCAGTTTTCCCTGTTTTCCACCACCCCACTCTTTTAATAATTGTATATACTGTACT  
 TGTCTACTTGCTTGTCTTTAAACAGGGGCCCCCACAGTTCACTCTCACTGTTAGATTT  
 TGCCTTTTCCAGGTATCCCCAACCTGCAATAAACTCTTCCCTCTTCAG

SEQ ID NO: 26\_AA383293\_H

CCAGCAGCCAAGAGGGTAGTGGTGTACCGGAATGGGGACCCATTCTTCCCAGGCTCCCAG  
 CTGGTGGTGAATCAACGCCGCTTCCCCACCATGGAGGCCTTCTCTGCGAGGTGACATCA  
 GCTGTGCAGGCCCCACTGGCTGTGCGTGCCCTCTACACACCTTGTATGGCCACCCTGTG  
 ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTTGAACGATTC

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FIGURE 2S

CACAAGCTCCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTTCAGGAATGGGGACCTGGTA  
AGTCCCCCATTTAGTCTGAAGCTGTCCCAGGCTGCCAGCCAGGACTGGGAACTGTGTTG  
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG  
GGGCTCCCCTGTGTGAGCAGGGAAGGAGCTGGTAACCTGGCCATTACTATGTGGCTGTGCGA  
GAGGATGAGTTCAAGGACCTTCCCTATCCAGCTCTGTCCACAAGAGGGCTCCTGGCAGCA  
GGCAATGAAGCCCACCTGAGGAGTGGAGTGGGGACTGTGCTGGTTCCCCCAAGCCTCTT  
GGAAGGAAGGCTAAGAAGGAGACATGCCTAATCGTGACCCTGACCCTGAAATACCAGCAG  
TCAGAAACAAGCAGAGACGGGCAATCATTTCCCATCAGGAGTTATAGGAGTATATGGAGCT  
CCCCACCGAAGGAAGGAGACAGCGGGGGCCCTGGAAGTAGCAGATGATGAAGACACTCAG  
ACAGAGGAGCCCTTGGATCAGAGGGCAGCACAGATAGTGAACAGGTTACTTGTCTGCAA  
GACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTTCTGTTATGCC  
CAAGATGACTTTGTCTCTGATCATAGTCGTGACGGCTCCTGAGAGAGCACCAGGCGGGC  
TTTGAGAAGCTCCGAGGACCCGAGGAGAAGAGAAGGAGGCAGAGAAGGAGAAAAAGCCA  
TGTATGTCTGGAGGCAGAAGGATGACTCTCAGAGATGACCAACCTGCAAAGCTAGAAAAG  
GAGCCCAAGACGAGGCCAGAAGAGAACAAGCCAGAGCGGCCAGCGGTGCGAAGCCACGG  
CCCATGGGCATCATTGCCGCCAATGTGGAAGGAGTGCAGACACCGCGAGACCAGGCAGGCCTATGCC  
GATGGGAACTTTGCTGTCTGTAAGGAGTGCAGACACCGCGAGACCAGGCAGGCCTATGCC  
ATGAAGATCATTGACAAGTCCAGACTCAAGGGCAAGGAGGACATGGTGGACAGTGAGATC  
TTGATCATCCAGAGCCTCTCTCACCCCAACATCGTGAAATTGCATGAAGTCTACGAAACA  
GACATGGAAATCTACCTGATCCTGGAGTACGTGCAGGGAGGAGACCTTTTTGACGCCATC  
ATAGAAAGTGTGAAGTTCCCGGAGCCCGATGCTGCCCTCATGATCATGGACTTATGCAA  
GCCCTCGTCCACATGCACGACAAGAGCATTGTCCACCGGACCTCAAGCCGGAAAACTT  
TTGGTTTCAGCGAAATGAGGACAAATCTACTACCTTGAAATTGGCTGATTTTGGACTTGCA  
AAGCATGTGCTGAGACCTATATTTACTGTGTGTGGGACCCCAACTTACGTAGCTCCCGAA  
ATTCTTTCTGAGAAAGGTTATGGACTGGAGGTGGACATGTGGGCTGCTGGCGTGATCCTC  
TATATCCTGCTGTGTGGCTTTCCCCCATTCGCGAGCCCTGAXXGAGGGGACCGAGCAG  
CTCTTTAATCATCCAGCTGGGCCACTTTGAGTTCTTCCCCCTTACTGGGACAATATC  
TCTGATGCTGCTAAAGATCTGGTGAGCCGTTGTGGTGGTAGACCCAAAAAGCGCTAC  
ACAGCTCATCAGGTTCTTCAGCACCCCTGGATCGAAACAGCTGGCAAGACCAATACAGTG  
AAACGACAGAAGCAGGTGTCCCCCAGCAGGATGGTCACTTCCGGAGCCAGCACAAGAGG  
GTTGTGGAGCAGGTATCATAGTCACCACCTTGGGAATCTGTCCAGCCCCAGTTCTGCTC  
AAGGACAGAGAAAAGGATAGAAAGTTTGAGAGAAAAACAATGAAAGAGGCTTCTTACATA  
ATTGGTGAATCAGAGGGAGAGACACTGAGTATATTTTAAAGCATATTAATAAATTAAGT  
CAATGTTAAATGTCAACATATTTTTAGATTTGTATATTTAAAGCCTTTAATAATTTT  
TGGGGGGTAAGCATTGTCTCAGTGAGGAATTTTGGTAATAATGATGTGTTTTGCTTCCC  
CTTTGTAACCAAGTTTATTCTGTACTACAGGAGTGGTGCTTACCAGGGTCTAAACTCCCC  
CTGTGAGATTAATAAGGTGCATTG

SEQ ID NO: 28\_AA197883\_M

ATGCCAACCGCGCCGGTCTGCGCCCGCCGCGCCAGCGACCCCCGCCCCGCGGCA  
CCCAGTCGCCCCTGCGCCTCCCATTCGGGCCACCGAGGCCCATGTGACCATTCTCTGAAA  
TGCTTAAGCTCGAAGATCTCTGAGAGAAAGCTGCCAGGCCCTGGTTACCTGCGGGACGA  
GGACCTCTGGAGAAGCCAGTTCTGGGGCCACGTGGTGCCGTGATGCCGTGTTACGCCCT  
CAGAGCAGCCTCCACTCAGTCCGCGCAGAGCACAGCCCACTGAAGCCAGGGTGGTGACG  
GTGGTGAAGCTGGGTGGGCAGCCCCCTCCGTAAGGCCACCTGCTCCTCAACCGGCGCTCA  
GTGCAGACCTTTGAGCAGCTCCTATCAGACATCTCCGAAGCCTTGGGCTTCCCACGCTGG  
AAGAACGACCGTGTGCGGAAGCTGTTACCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT  
GACTTCTTCCGGGAGGGTGATGCTTTTATAGCTATGGGCAAAGAGCCGCTGACATTGAAG  
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCGGGCTCTTGCCCTGGCCCCCT  
CACAGTAGAGTCCCCCAGGCTGAGAAGCAGACTTCCAGCAAGCTTCTGAAAGGA

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FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT  
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCAGAAG  
TGGGTAAGAGGGAAACAGGAGTCAGAACCTGGTGGCCCCGCTTCACCCGGGGCAGCCACT  
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCT  
GGGAGATTGTGAGATGTGAGAAGTGTAAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG  
AGGGAGCCGTGCCCGCTGGGAACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT  
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT  
GGAGAGGAAGGGTGAAGGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA  
ATGAGGAGGCCCAACAGCAACTCAGACAAGAAAGAGATCAGAGGCTCAGAAAGTCAGGAC  
AGTTATCCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA  
GAGGAGGGGGCCGATAGACATGAGGAGAGAGGACCGGCACACATGCAGGAGCAGCATGCC  
GCCTGGCTCCGGAGAGAGCAGCAGGCCGAACCCCCACAGCTCCCCAGAACCCGAGGGGAG  
GAGAAGCAAGCAGAGCACGAGAAGAAGCCAGGCGGCTTAGGAGAGAGGAGGGCGCCAGAG  
AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG  
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTCATT  
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC  
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTGACAGTGTAG  
ATTTTAATCATCCAGAGTCTCTCATCCCAACATTGTGAAACTGCATGAGGTCTACGAA  
ACGGAGGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTGATGCC  
ATCGTTGAAAATGTGAAGTTTCCAGAGCCCGAGGCTGCAGTTATGATCACAGACTTGTGT  
AAGGCCTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC  
CTCCTGGTTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG  
GCCAAATATGTGGTGAGGCCTATATTTACTGTGTGTGGGACGCCAACATATGTAGCTCCT  
GAAATTCTTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC  
CTATACATCCTCTTGTGTGGCTTCCCCCCTTTCGGAAGTCTTGAGAGGGACCAAGACGAG  
CTCTTCAACATCATCCAAGTGGGCCAGTTTGAGTTCCTCTCTCCTTACTGGGACAACATT  
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCCTAAGAAGCGGTAC  
ACGGCCGAACAGGTCCTACAGCATCCCTGGATTGAGATGGTTGGGCATACCAACACAGGG  
AACTCACAGAAGGAGGAGTCCCCCAACAGTTTAGGTCACTTCCAGAGTCAGCACAAGAAG  
GTTGCAGAGCAGATGCCATAA

SEQ ID NO: 29\_DRAK2\_H  
CTCCGCTGCTGTGCGCCAGGAGTCACTTCACGAGAAGCCAGGTCACAACCGTCGGCCCTTG  
TCTGGAAGTAAGAGTGGATCCTGCCACGTTCCGAGCTCCCTGGCGCCTCGCCCGGCTG  
GAGCTAGAGAACTCGTCTGTGGCGGCCCCCGGCGTGGGGCGGGACAGCGGCCCCCTGGA  
GGGGGCAGTCCCGGGAGAACCTGCGGCGGCGGAGCGGTAAAAATAAGTGAATAAGAAG  
CAGACCTGGGAATCACCTAACATGTGAGGAGGAGATTGATTGCCGAAGTATTTAGGC  
CTACTAACTACAACCTCCTCAAATTTCAATAAAAAATGGAAAACTTTAATAATTTCTATATA  
CTTACATCTAAAGAGCTAGGGAGAGGAAAAATTTGCTGTGGTTAGACAATGTATATCAAAA  
TCTACTGGCCAAGAATATGCTGCAAAATTTCTAAAAAAGAGAAGAAGAGGACAGGATTGT  
CGGGCAGAAATTTTACACGAGATTGCTGTGCTTGAATTGGCAAAGTCTTGTCCCCGTGTT  
ATTAATCTTCATGAGGTCTATGAAAATACAAGTGAATCATTTTGATATTGGAATATGCT  
GCAGGTGGAGAAATTTTACGCTGTGTTTACCTGAGTTGGCTGAAATGGTTTCTGAAAAT  
GATGTTATCAGACTCATTAAACAAATACTTGAAGGAGTTTATTATCTACATCAGAATAAC  
ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCCTCTCGGG  
GACATTAAATAGTAGATTTTGAATGTCTCGAAAAATAGGGCATGCGTGTGAACCTCGG  
GAAATCATGGGAACACCAGAATATTTAGCTCCAGAAATCCTGAACTATGATCCCATACC  
ACAGCAACAGATATGTGGAATATTTGGTATAATAGCATATATGTTGTTAACTCACACATCA  
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT  
TATTCGGAAGAACTTTTTCATCAGTTTTCACAGCTGGCCACAGACTTTATTACAGGCCTT



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## FIGURE 2U

TTAGTAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA  
CAGCAGTGGGACTTTGAAAACCTGTTTCACCCTGAAGAAAACCTCCAGTTCCTCTCAAACCT  
CAGGATCATTCTGTAAGGTCCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC  
TGTGGTGTAGAGAAGACAAAGAGAATATCCCAGAGGATAGCAGCTGTTGTTTCCAAAAGA  
TTTCGTTTCGATGACTCATTACCCAATCCCCATGAACTTGTTCAGATTTGCTCTGTTAG  
CACTTTTTTCTTTGACTCATTGGACTGAATTTGAAATTTTATATCCACTCCAGTGAGAT  
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACTTTTCCATGGAATA  
ATTTAGGGAAGTGTTTTAAATGTTAAATTAAGTGTGCTAGCATGTTATGATTTTCATATCC  
TGAGATAGCTCTGCAGATAAGAAAATATTTAAATATATGACAAAAGTAAATTTGTACAT  
GTGAAAG

SEQ ID NO: 30\_W44160\_M DRAK2\_M  
CCAGACGCGGCTGCACTTTTCAAACCTCAACTGTAAGAAGCGTCGGTCAGCGTCTGTGCG  
GTCGCCGCGGGAGTCCGCTCACAGGGGCTGGCTGACGGCGACCAGCCGTTGTGGGGAA  
GAGTGGCAGGTAAGTCTGCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA  
GGAGATTCGATTGCCGAAGTGTCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA  
AAACAGAGAATTTTAATAATTTCTATACTCTTACCCCAAAGAACTGGGAGAGGAAAAT  
TTGCTGTGGTTAGACAATGTATATCAAATCAACTGGACAAGAGTATGCTGCCAAATCCC  
TGGAGCTGGCCAGGTCTTGTCCCCACGTGATTAATCTGCATGAGGTCTACGAAAATGCAA  
CGGAAATCATTGTTGGTGTAGAAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC  
CTGAGTTAGCCGAAATGGTATCTGAAAATGATGTTATCAGACTCATTAAACAAATCCTTG  
AAGGAGTTCATTATCTACATCAGAATAACATTGTTTACCTTGATTTAAAGCCACAGAATA  
TACTTTTGGAGCAGTATATACCCACTCGGGGACATAAAAATTTGTAGATTTTGGAAATGTCTC  
GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC  
CAGAAATCCTCAACTATGATCCCATTACCACAGCAACAGATATGTGGAATATTGGCATAA  
TAGCGTATATGTTGTTAACTCATACATCACCATTGTTAGGAGAAGATAATCAAGAAACAT  
ATCTGAATATTTCTCAAGTGAATGTAGATTATTCAGAAGAAATGTTTTTCATCAGTTTCAC  
AGCTGGCCACAGACTTCATCCAGAGCCTTCTAGTAAAGAACCAGAGAAAAGACCAACAG  
CAGAATCCTGCCTATCCCCTCATGGCTGCAGCAGTGGGACTTTGGAAGCTTGTTCATC  
CTGAGGAACTTCAGGCTCCTCTCAAATTCAGGATCTGACTCTCAGGTCCTCTGAAGAGA  
AGACCTCCAAGTCTCCTGTAATGGGAGCTGTGGAGCCCGGGAGGACAAGGAGAACATCC  
CTGAAGATGGCAGCTTAGTTTCTAAAAGATTTTCGATTGCTGACTCATCTGGACTGACT  
ATGAACTTGTTCAGATTTGTTCTGTTAGCATTTTCTCTGTGACTCATCTGTTTATAT  
CGGAAATTTGAAATCTCTGCTTAGAAGAACTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG  
TATAAATGCACTTCTGCTTAGAAGAACTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG  
GCTAGCATATCATTCTTGTCTGAAATTTGTTTGCAGAGGAAATATTTAAGTATATGA  
CAAAAAATGTAAATTTGTGTTTAAAGAGAACACATGCAACTGAAAGAACTCAAGTTCAGTCA  
GACTTATAAAATGGGTTATATTATGGTTAGTAAAGTTGAAAAAAATGAAAACAGGAAT  
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA  
AATGCTGTCAAGGGTAAACCACAACATATACTGCTTTATAAATACTCCAGAGAGAGTTTA  
TAGTTGAAAGTATTTCCAGTTACCAATAATAGCTTGAAACTGTAAGATTTTCTTTGTGT  
GCCATGTGCTCGGTGAGAGGACACAGTCAACCAGAGCAGGTTGATCCAGGCTGTTTCTC  
TGCAAACCGAGTCAAACTCGACATCATTTCCAGCTCATGTATTTTGTACGTGCATCATA  
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAAATAAGAGGCCTTTGTCTTCTAGA  
ATGATTAGAGTAGAGGAGAATTGGATAGTACAGAATATGCTCTAGTTTCAGTCAGACATA  
TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTGGATGTCTCCTAAGTCT  
CAGGATAGAAGCCCATCATTAGAGCATAGGCACTTCAGGAATTTCTGTGTGAAATTTCTAG  
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA  
CACAAACATGGGAGTGTTCAGTGTGTCCGTGGTCAATATCTATGTTTCAGTCCTGATGG

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## FIGURE 2V

GAGGGGCTAGGGACTGCTTTGGAGATTTCCCACTGGTGTCCATTTTAAGGTCTGTAATA  
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA  
ACAAATTTAAAGCCTGTGTATTGAAGTGGGTGTTAGTCTAACAACCTGTAAATTCTTGAA  
ATTGTTACTAAAATTCCAAATTCFTTAGATAACTTTAAACTATTTAAATTGAGCATTGCT  
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTATTATTTTAAAGGAAAAGTTGT  
TTGCCCTTTGTATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT  
GATAGATAAAATACAGCCTTTAAACAACCTC

SEQ ID NO: 31\_H01248\_H, DRK1\_H

ATGATCCCTTTGGAGAAGCCAGGCAGCGGCGGCTCCTCCCCAGGCGCCACCTCAGGCTCG  
GGCCGGGCGAGCCGGGGTCTGAGCGGGCGGTGCCGGCGCGCGCGCCGCCCCAGGCCCCG  
GGGCTGCTGACAGAGATACGCGCCGTGGTGCGCACCGAGCCCTTCCAGGACGGCTACAGC  
CTGTGCCCGGGCCGGGAGCTGGGCAGGGGGAATTTGCAGTGGTGAGAAAATGTATAAAG  
AAAGATTCTGGGAAAGAATTTGCTGCAAAGTTCATGAGAAAAGAAGAAAAGGCCAAGAT  
TGTGCGATGGAAATAATTCATGAGATTGCTGTACTTGAAGTAGCACAAGACAATCCTTGG  
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT  
GCTGCTGGGGTGAAATCTTTGACCAAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA  
AAAGATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTTACACACTCGT  
GATGTAGTTCATCTTGATTTGAAGCCTCAGAATATTCTGTTGACAAGTGAATCTCCATTG  
GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC  
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATTCTTAGTTATGATCCTATA  
AGCATGGCAACAGATATGTGGAGCATTTGGAGTGTAAACATATGTCATGCTTACAGGAATA  
TCACCTTTCTTAGGCAATGATAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA  
AGTTATTCTGAGGAAGAATTTGATGTTTTGTCTGAGTGGCTGTTGATTTTCATCAGGACA  
CTTTTAGTTAAGAAACCTGAAGATCGAGCCAGTCTGTAAGAATGTCTAAAGCACCCCTGG  
TTGACACAGAGCAGTATTCAAGAGCCTTCTTTCAGGATGGAAAAGGCACTAGAAGAAGCA  
AATGCCCTCCAAGAAGGTCAATCTGTGCCTGAAATTAATTTCGGATACCGACAAATCAGAA  
ACCGAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAA  
TGCAGACAGTCTGAAAAAGAGAAAATGGAGCAAAAGGCCATTTCCAAACGATTTAAATTT  
GAGGAACCTTTGCTACAAGAAATTCAGGAGAATTTATCTACTGA

SEQ ID NO: 32\_AA021445\_H

CGGGGCTGCCGGGGCCGGGACTGGGGGAGCCGGGCCCCGGGGCCGCTGCTGCCTCCGCC  
CGCGCCGGGGTCCCCAGCCGCCCCCGCTGCCGTGTCCCTGCGGGCCGGCCAGCCGCTCC  
CCCAGCCCCGGCCTCCCGCGGACCCATGCCCGCCGTATCGGCTACTACGAGATCGACCG  
CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC  
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACCTGAAGAAGAT  
TTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCATATCATCAGGCTCTACCA  
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT  
ATTTGACCACCTGGTGGCCCATGGTAGAATGGCAGAAAAGGAGGCACGTGCGAAGTTCAA  
ACAGATCGTCACAGCTGTCTATTTTTGTCACTGTGCGGAACATTGTTTCATCGTGATTTAA  
AGCTGAAAATTTACTTCTGGATGCCAATCTGAATATCAAAATAGCAGATTTTGGTTTCAG  
TAACCTCTTCACTCCTGGGCAGCTGCTGAAGACCTGGTGTGGCAGCCCTCCCTATGCTGC  
ACCTGAACTCTTTGAAGGAAAAGAATATGATGGGCCCCAAAGTGGACATCTGGAGCCTTGG  
AGTTGTCTCTACGTGCTTGTGTGCGGTGCCCTGCCATTTGATGGAAGCACACTGCAGAA  
TCTGCGGGCCCCGCTGCTGAGTGGAAAGTTCCGCATCCCATTTTTATGTCCACAGAATG  
TGAGCATTGATCCGCCATATGTTGGTGTAGATCCCAATAAGCGCCTCTCCATGGAGCA  
GATCTGCAAGCACAGTGGATGAAGCTAGGGGACGCCGATCCCAACTTTGACAGGTTAAT  
AGCTGAATGCCAACAACTAAAGGAAGAAAGACAGGTGGACCCCTGAATGAGGATGTCCT  
CTTGGCCATGGAGGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

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## FIGURE 2W

TGCCTATGATCACTATAGTGAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA  
AACCTTGCCTCTCGGAGCACTTCTAGCATGCCCCGAGCCCTGGCCTTTCAAGCACCAGT  
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT  
GATCAACCCAGAGAACCAAAATTGTGGAGCCGGATGGGACACTGAATTTGGACAGTGATGA  
GGGTGAAGAGCCTTCCCCTGAAGCATTGGTGGCTATTGTCAATGAGGAGGCACACAGT  
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT  
TCCTGGAGTCAACCCCCAGGCTCCATTCTGCAGGTGGCCCCCTAATGTGAACTTCATGCA  
CAACCTGTTGCCTATGCAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC  
TCTCTACAGCCGCCCACGCTACAGCTGTTGAATGGAATGGGCCCCCTTGGCCGGAGGGC  
ATCAGATGGAGGAGCCAAACATCCAACCTGCATGCCCAGCAGCTGCTGAAGCGCCCACGGG  
ACCCTCTCCGCTTGTCAACATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA  
GAGCTCAGACGGGAGCCAGACCAGGAAGCTGTGCAGAGGTACTTGGCAAATAGGTCCAA  
AAGACATACTGGCCATGACCAACCTACAGCTGAGATCCCACCGGACCTACAACGGCA  
GCTAGGACAGCAGCCTTTCCGTTCCCGGGTCTGGCCTCCTCACCTGGTACCTGATCAGCA  
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCCTGT  
GCGCCGGTTCTCAGATGGGGCTGCGAGCATCCAGGCCTTCAAAGCTCACCTGGAAAAAT  
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA  
CGGGGGGAGATTGATGAAAGAACCCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA  
GCAGGAGCAGCACCATCAAATTTCTCCAGCAACAATTCAGACTCTATCTGTCTCTCTCA  
GCCATCTCCACCTCTTCAGGCTGCATGTGAAAATCAGCCAGCCCTCCTTACCCATCAGCT  
CCAGAGGTTAAGGATTTCAGCCTTCAAGCCCACCCCCAACCCACCCCAACAACCATCTCTT  
CAGGCAGCCAGTAATAGTCTCTCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC  
TGCACTCTCTTCCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC  
TGAGAAGTGTCTCTCTCTCCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC  
TCAGTCACAGCAGGTACCATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC  
AGGCACAGCTGCAGGCTCCAGTGGGCGCGCATCTCCATCAGCCCCAGTGTGGTTCAGAT  
GCAGATGCAGCACCGTACCAACCTGATGGCCACCCTCAGCTATGGGCACCGTCCCTTGT  
CAAGCAGCTGAGTGTGACAGTGCAGAGGCTCACAGCTTGAACGTGAATCGGTTCTCCCC  
TGCTAACTACGACCAGGCGCATTTACACCCCATCTGTTTTCGGACAGTCCCGGGGTTTC  
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTTCTCTCCAACCCAGCCCTGAAAGT  
CCCTCCACTTGACCAATTCCCCACCTTCCCTCCCAGTGCACATCAGCAGCCGCCACACTA  
TACCAGTCCGCACTACAGCAGGCTGCTGTCTCCCACGCCGAGCTATACAAGACA  
CCAGCAGGTACCCCATCTTCAAGGACTGCTTTCTCCCCGCGCATTGCTCACCGGCCA  
CTCGGACATCCGGCTGCCCCAACAGAGTTTGACAGCTCATTAAAAGGCAGCAGCAACA  
ACGGCAGCAGCAGCAGCAACAGCAGCAACAGCAAGAATACCAGGAAGTGTTCAGGCACAT  
GAACCAAGGGGATGCGGGGAGTCTGGCTCCCAGCCTTGGGGACAGAGCATGACAGAGCG  
CCAGGCTTTATCTTATCAAAATGCTGACTCTTATCACCATCACACAGCCCCCAGCATCT  
GCTACAAATCAGGGCACAAGAATGTGTCTCACAGGCTTCTTACCCACCCCGCCCCACGG  
GTATGCTCACCAGCCGCACTGATGCATTGAGAGCATGGAGGAGGACTGCTCGTGTGA  
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAAGGTGCCA  
TGACAGCCCTCTGCTCTTGAGTACCGGTGGACCTGGGGACCTGAATCTTTGCTAGGAAC  
TGTGAGTCATGCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAACCTGCTGCATT  
CAGTAAAAATAAGGTGCCCAGCAGAGAGCCTGTATAGGGAAGTGCATGGATAGAAGTTC  
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCACGCCCTC  
CGTCCATGAGCACCAAGGCCCGGGCCCTCCAGAGACACCACAGTCCAGAACAGCGA  
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT  
TAGCTCTGCCCCGATGTCCGATGCAGTTCTCAGTCAGTCTTCGCTCATGGGCAGCCAGCA  
GTTTCAGGATGGGGAAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTATGAGCACCCAGA  
CCTGAGTGATGGCAGCCAGCATTTAACTCCTTGTCTATCCATCTACGTGTATTACAGA  
CATCTGCTCAGCTACAAGCACCCGAAGTCTCCTTACGATGGAGCAGGCAGGCGTGTA

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## FIGURE 2X

ACAAGAAACAGAGAGTTTTGTGTACAGCTTGGGAATGAAAAGGTTGATTGTAAACCCACA  
 GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC  
 TGCTTTCTCACATTTGGTTTCATCCGTGTGCTGTTCTTTTGGGTTCTGAGAGGGTTTTGC  
 CATGTTTGCTTGTATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC  
 C

SEQ ID NO: 33\_2R22-5-11\_H

CTGGGCCGCTGCCGCTCAGGTCGGCCGCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA  
 GGGCGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC  
 AGCGCGCCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG  
 AACCAGCCAAATTTTCGAGACAGCTCACGGCTTAGAGGAAGGTTTCATCTAAATAAAGGCC  
 GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCCTGTGTGACCAGAAGGCT  
 TATTTGCAAGTTTCTTCTTCCCTGGGGTCCAGATTATTAGGTCTCCAGCGCCCTGCAGCT  
 TGACAGAAAGAGAAGCATGAAATGAAGGTGAGAGATGAGATCCCGCAGCAGGGACGTGGG  
 GGCCTCCCGAGGGGCATTTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAATAG  
 CAAACAGAAGCCTTTGTCTCTGGGCGACAGCCACCTACCACAAAGCATCAGACTCCACGTC  
 TGGCCAGAAAGTTCTGGAGTCCCATCAGGCCAGTGGGTATGTAACATGTGCCTAATTGT  
 ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG  
 CAGCTCCTGGCTGGGCTGGGCGAGCTCAGCTACCAGTTCACTGCCTTCTCTACTAAA  
 GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAACTCTTTTGAACCTGGGCACCTGTCTGT  
 CCTCAGTTGGCATCTCCACCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG  
 CTGAGATGGAGACGTGAGCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC  
 CTGGTGAACCCCCACTATGCCCGGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTGAG  
 ACCGAGAGTAGCAAGGAGGGTGAGGAGGACAGCCCCGCGAGCTGACGCCCTTCGAGAAA  
 CTGACACAGGACATGTCCAGGATGAGAAGGTGGTGAGGGAGATCACGCTGGGGAAACGG  
 ATAGGCTTCTACCGAATTCGAGGGGAAATCGGAAGTGGAACTTCTCCCAAGTGAAGCTT  
 GGGATTCACTCCCTAACCAAGAAAAGGTGGCCATTAAGATCCTGGACAAGACCAAGTTA  
 GACCAGAAAACCCAGAGGCTACTATCCCGAGAAATCTCCAGCATGGAAAAGCTGCACCAT  
 CCAACATCATCCGCCTTACGAAGTGGTGAGACCCTATCCAAGCTGCACTTGGTGATG  
 GAGTATGCAGGGGGTGGGGAGCTCTTCGGAATAATAGCACTGAGGGGAAGCTCTCTGAA  
 CCAGAAAGCAAGCTCATCTTCTCCAGATTGTGTCTGCCGTGAAGCACATGCATGAAAAC  
 CAAATTATTATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG  
 AAGGTGGGCGATTTTGGATTACGACAGTAAGCAAAAAGGTGAAATGCTGAACACTTTC  
 TGTGGGTCTCCTCCCTACGCTGCGCCTGAACTCTTCCGGGACGAGCACTACATCGGCATT  
 TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGAAGTGGCACCATGCCA  
 TTTCCGGGCAGAAACCGTGGCCAACTAAAAAAGAGCATCCTCGAGGGCACATACAGTGTA  
 CCGCCGACGTGTGAGAGCCCTGCCACCGACTCATCCGAGGAGTCTTCAGCAGATCCCC  
 ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC  
 CCTACACCTTTGGAACCTTTCCAAGTGGATCCCAACATTGTGCGGAAACCGCACTCTC  
 AAGGAAGAAGAAAATGAGGTCAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT  
 ATTCGAAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT  
 TTACATAGAGTCCAAAGGAAGAAGGCTTTGGAAAGTGTCCAGTCATGATGCTACCAGAC  
 CCTAAAGAAAGAGACCTCAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC  
 AAATTTTGCTCGATTTTATAAATTGCACTAGACTGCTTGTAACTAACCAAGATGATTGTT  
 GCTGCTTCTAAATTTTTTCAAGGACAACCTGAGTGGAGACATTTTGTAAATTTTAAAT  
 AAACCTAAATTTGAGATATGCAAAAAAAA

SEQ ID NO: 34\_R31237\_1\_H, AAC33487

ATGTCCACTAGGACCCCATGCCAACGGTGAATGAACGAGACACTGAAAACCAACAGTCA  
 CATGGAGATGGGCGTCAAGAAGTTACCTCTCGTACCAGCCGCTCAGGAGCTCGGTGTAGA

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## FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAACTACAGACTGTTGAAA  
ACAATCGGCAAGGGGAATTTTGCAAAAAGTAAAATTGGCAAGACATATCCTTACAGGCAGA  
GAGGTTGCAATAAAAAATAATTGACAAAACCTCAGTTGAATCCAACAAGTCTACAAAAGCTC  
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATGCCAATATAGTGAAGTTATTGAA  
GTCATTGAAACTGAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA  
TTTGACTATTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA  
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG  
GCTGAAAATCTATTGTTAGATGCCGATATGAACATTAAAATAGCAGATTTTCGGTTTTCAGC  
AATGAATTTACTGTTGGCGGTAACTCGACACGTTTTGTGGCAGTCCTCCATACGCAGCA  
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGGCCAGAAGTGGATGTGTGGAGTCTGGGG  
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTAAAGGAA  
CTGAGAGAGAGAGTATTAAGAGGGAAATACAGAATTCCCTTCTACATGTCTACAGACTGT  
GAAAACCTTCTCAAACGTTTCTTGGTGCTAAATCCAATTAAACGCGGCACTCTAGAGCAA  
ATCATGAAGGACAGGTGGATCAATGCAGGGCATGAAGAAGATGAACTCAAACCATTTGTT  
GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT  
TCACAAGAAGAAATTCAAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA  
TATTTGTTATTGGGGAGAAAATCTTCAGAGCTGGATGCTAGTGATTCCAGTTCTAGCAGC  
AATCTTTCACTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT  
CCTCACCACAAAGTGCAGAGAAGTGTCTTCTCAAGCCAAAAGCAAAGACGCTACAGTGAC  
CATGCTGGACCAGCTATTTCCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT  
GCAGATGGTGACCTCAAAGAAGATGGAATTTCTCCCGGAAATCAAGTGGCAGTGCTGTT  
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG  
GCGGATATTCTGAAACGCAAGAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT  
GGAATGACACGACGAAATACTTATGTTTGCAGTGAGAGAACTACAGCTGATAGACACTCA  
GTGATTGAGAATGGCAAAGAAAACAGCACTATTCTGATCAGAGAACTCCAGTTGCTTCA  
ACACACAGTATCAGTAGTGCAGCCACCCAGATCGAATCCGCTTCCCAAGAGCACTGCC  
AGTCGTAGCACTTTCCACGGCCAGCCCCGGGAACGGCGAACCAGCAACATATAATGGCCCT  
CCTGCCTCTCCAGCCTGTCCCATGAAGCCACACCATTGTCCAGACTCGAAGCCGAGGC  
TCCACTAATCTCTTTAGTAAATTAACCTCAAACCTCACAAGGAGTCGCAATGTATCTGCT  
GAGCAAAAAGATGAAAACAAAGAAAGCAAGCCTCGATCCCTACGCTTACCTGGAGCATG  
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAAATCCGCAAGTGTTGGAC  
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT  
GGGCACGCGGAGAACCTCGTGCAAGTGGGAAAATGGAAGTGTGCAAGCTGCCAAGACTGTCT  
CTGAACGGGGTCCGGTTTAAAGCGGATATCGGGGACATCCATAGCCTTCAAAAATATTGCT  
TCCAAAATTGCCAATGAGCTAAAGCTGTAA

SEQ ID NO: 35\_W90839\_M  
AAAGGGCCGTCTGGTCCAGCCGTTCCCTGGGTGCCCCGTTGCCGGAACCTCTATCGCTTCC  
TGCCCTGAGGAACAACCCCATGTGGGCAACTATAGGCTGCTAAGGACCATCGGGAAGGGC  
AACTTCGCCAAAGTCAAGCTGGCTCGGCATATCCTCACGGGCCGGGAGGTGCTATTAAG  
ATCATTGATAAGACCCAGCTGAACCCAGTAGCTTGCAAGCTTTTGGAGGTGATAGAGACGGAG  
ATTATGAAGGACTCAACCACCCCAACATCGTGAAGCTTTTGGAGGTGATAGAGACGGAG  
AAGACGCTATACCTGGTGATGGAATACGCTAGCGCAGGAGAAGTGTGACTACCTCGTG  
TCGCACGGCCGCATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTCAGCC  
GTGCACTACTGTATCAGAAGAACTTGTACACAGGGATCTAAAGGCTGAAAACCTGTTG  
CTGGATGCCGAGGCCAACATCAAAATCGCCGACTTCGGCTTACGAATGAGTTACGCTG  
GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCATACGCCGCCAGAGCTGTTCCAG  
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTCATCCTGTACAG  
CTGGTCAGCGGCTCCCTGCCCTTCGATGGGCACAACCTCAAGGAGTGGGGAGCGAGTC  
CTCAGAGGAAAGTACCGGTTCCCTTCTACATGTCTACAGACTGCGAGAGCATTTCTGCGG

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FIGURE 2Z

AGATTTCTGGTGCTGAACCCCGCAAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA  
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG  
CGGATGCCGGGTTCGGAAAGCGAGCTGCAGTGCACTGGGCAGTGGAAGTCGAGGCTTGCCC  
CCCTCCAGCCCCATGGTCAGCTGCCCCACAACCCCAATAAGGCAGAGATCCCTGAGCGG  
CGGAAGGACAGCACTAGCACCCCTAACAACTCCCCCCCAGCATGATGACCCGAAGAAAC  
ACCTATGTGTGCACAGAGCGACCAGGATCTGAACGCCCGTCCTTGTGCGAAATGGCAAA  
GAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCCAGTCATAGCCTGGCT  
CCCCCGTCAGGCGAGCGGAGCCGCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT  
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGCGGGGGGTGTGCAGAATGGA  
CCCCAGCCTCACCCACGCTTGCCACAGGGCCGACCCCTGCCCTCCGGGCGGCCTCGC  
CCCACCACCAACCTCTTACCAAGCTGACCTCCAACTGACCCGAAGGGTCACAGACGAA  
CCTGAGAGAATCGGGGGACCTGAGGTCAAACTTGCCATCTACCTTGGGATAAAACGGAA  
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC  
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

SEQ ID NO: 36\_406786.5\_H

GTAGCCGGCTTGGCGTGACCGTCGCCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT  
GGCCTCCCTTCTTCCCATGGAGGTTCGGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG  
CCTTTCCAGAGCCTCCCTTGCCAGTGTGAGCAGAGGGCCAGCTGCACAGACCACTGC  
TGAGCCCAGCAGGTCTTTTTCTCAGCCACAGACACCTGAGCAGAAGGAATGGGCTTTTC  
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC  
ATCACTGGCTGCCCAGAATATTTGTACAAGTAACTGCACTGCCCTGCTGCCCTGAGCA  
CACGGACCCGTCCGAACCGGGGCGAGTGTCTCTGCTGCTGCCCTGCTGCCGGGACTGTC  
CTCAGGGTGGTCTCACCTCTGCTTCCGGCCCCCTGTGTGCAACCCCTAACAAAGGCCATCTT  
CACGGTGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGCGGGCTCCT  
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTTCTTTCTGAGGTGAGA  
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGGCCAGGCCACGCTGCGGT  
GGTGTTTGGCACGGTGGTGGACATCATACCCGTAGTGGGGAGAAGATTCCAGTGTCTGT  
TGGATGAAGAGGATGCGGCAGGAGCGCCGCTATGCTGCGTGGTGGTCTGGAGCCCGT  
GGAGAGGGTCTCGACCTGGGTGCTTTCCAGAGCGATGGCACCATCACGTCATGTGACAG  
TCTCTTTGCTCATCTTACGGGTACGTGTCTGGGGAGGACGTGGGTGGGCAGCATATCAC  
AGACCTGATCCCTTCTGTGCAGCTCCCTCCTTCTGGCCAGCACATCCCAAAGAATCTCAA  
GATTGAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT  
GAAATCCCAACCCAGCAGCGAGGAGGCGACACCGGTGAGGCGGCCCCCTGTAGCGGCTA  
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCTCCTGCCGATGG  
GACCATCCACGGCATCAACCACAGCTTCCGCGTGAACCTGTTTGGTTACGGAAGACGGA  
GCTCCTGGGCAAGAATATCACTTTCCTGATTCTGCTGTTTCTACAGCTACATGGACCTTG  
GTACAACAGCTCATTACAGCTCCAGACCTGGCCAGCTGCCCTGGACGTCGGCAATGAGAG  
TGGGTGTGGGGAGAGAACCCTTGGACCCGTGGCAGGGCCAGGACCCAGCTGAGGGGGGCCA  
GGATCCAAGGATTAATGTCTGCTTGTGCTGGTGGCCACGTTGTGCCCGAGATGAGATCCG  
GAAGCTGATGGAAGCCAAGACATCTTACCCGGGACTCAGACTGAGCTGATTGCTGGAGG  
CCAGCTCCTTTCTCCTCTCACCTCAGCCTGCTCCAGGGGTGGACAATGTCCAGAAGG  
AAGCCTGCCAGTGCAAGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCTTGGG  
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGGAGAAAGCAGGTC  
TGAACAGTGGATGTGAAGCCATTTGCTTCTGCGAAGATTCTGAAGCTCCAGTCCCAGC  
TGAGGATGGGGCAGTGTGCTGGCATGTGTGGCCTGTGTGAGAAGGCCAGCTAGAGCG  
GATGGGAGTCAGTGGTCCAGCGGTTAGACCTTTGGGCTGGGGCTGCCGTGGCCAAGCC  
CCAGGCCAAGGGTCAGCTGGCGGGGGGAGCCTCCTGATGCACTGCCCTTGCTATGGGAG  
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGGCCCCCAGCCCCCTTGGGATGGCAGG  
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAACGACCGAGA



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FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCAGTTGAGCCTTGACAGGAGCCCT  
GGATGTCCCCACGCCGAACCTCGTTCCGACAGAGTGCCAGGCTGTACCGCTCCTGTGTCT  
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG  
CTATGCCTTGGCCACGGACCTCCCTGGGGGCTGGAAGCAGTGGAGGCCAGGAGGTTGA  
TGTGAATTCGTTTTCTGGAACCTCAAGGAACCTCTTTTTCAGTGACCAGACAGACCAAC  
GTCATCAAATTGTTCTGTGCTACGTCTGAACTCAGAGAGACACCCTCTTCCTTGGCAGT  
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTCTGTGTCTTGGATGACAG  
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGGCCAAGGCCGACGGTTCCGGGA  
GAGCTGTGTGGACATGATCCAACAGAACCGCTTGAGGTTTGTGTTGGTGTCTCTGAGCA  
TTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTCTTCCACGTTGGATGCTGGCCC  
TGAGGACAGTGGCCATCAGCAGAGGAGCCAAGGCTGAACGTCCAGGTCACCTCCACGCC  
CGTGATCGTGATGCGCGGGGCTGCTGGCCTGCAGCGGGAGATCCAGGAGGGTGCCTACTC  
CGGGAGCTGTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT  
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAGACCTCCTCCACAG  
CCAACGCGACTCAGCCGCCAGGACCCGCTGTTCTTGGCAGCCTGCCCGGCTCCACCCA  
CTCTACCGCTGTGAGCTCACCAGACCCAGCCTGGTGGAAAGTGCTCAGAGCCAGACCTG  
GTTTGAGGAGCCCCCAAGGCTGTGGAACGGAGGGGTTGGCGGCTGTGAGGGCGAGTA  
CTCCCAAAGTACAGTACCATGAGCCGCTGGGAGGTTGGGCGCTTCGGCTTCGTGTGGAC  
TGCTGTGGACAAGGGAACCAAGGAGGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT  
CTTGAGGATTGTTGGATTGAGGATCCCAAACCTGGGAAAGTTACTTTAGAGATCGCAAT  
TCTATCCAGGGTGGAGCACGCCAATATCATCAAGGTATTGGATATATTTGAAAACCAAGG  
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA  
CCGCCACCCAGGCTGGATGAGCCCTGGCGAGCTACATCTTCCGACAAGTGAGAGCAGG  
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCAATCAAGCTGATAGACTTTGG  
CTCGGCCGCTACTTGGAAAGGGGAAATATTTTATACCTTTTGTGGGACCATGTGGTC  
CTGTGCACCGGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGGAGCTGGAGATGTGGTC  
TCTGGGAGTCACTCTGTACACGCTGGTCTTTGAGGAGAACCCCTTCTGTGAGCTGGAGGA  
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCCAAAGAACTCATGAGCCTTGT  
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCACCACCTTGGAGAAGCTGGTGACAGA  
CCCGTGGGTAAACACAGCCTGTGAATCTTGCTGACTATACATGGGAAGAGGTGTTTCGAGT  
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGAGCCT  
GAGTGATGTGGCCAGGCTCAGGAGCTTTGTGGGGGCCCCGTTCCAGGCGAGGCTCCTAA  
TGGCCAAGGCTGTTTGCATCCCGGGGATCCCGTCTGCTGACCAGTAAACACCAATTTCT  
TTCCTGCTTTTCTCCACTTGGTTTGGAAATCACACAGTTTTTCAGGCTCCATCTGTTTG

SEQ ID NO: 37\_AA544838\_M 406786\_M  
CCACGCGTCCGCATCCCTGCTTGGATGAGCCCCTGGCGAGTTTCATCTTTGACAACCTAG  
TGCTGCTGTAGGATACCTGCACTCCCAAGGCATCATCCATAGAGACATCAAGGATGAGA  
ACATTGTGATTGCTGAGGACTTCAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT  
TAGAGAGGGGCAAACTATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG  
TTCTCATTGGAAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTCAACC  
TGTACACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG  
TTATTCATCCCCATTCCTGGTTTCCCAAGAACTTATGAGTCTTCTGTCTGGAAGTGTGC  
AGCCTTGGCCTGAGCAGCGGACCACTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC  
AGCCTGTGAACCTTGTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA  
GTGGCCTGCTGTGAGCTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC  
AGAGAGAGGGTCTCTGTGGGCTCCTGCTCCAGGGAGACTCGTGGTGACCAGCACTGCT  
TGCATCTTAAGGACCCCTCTTTGCCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG  
GGCAGTTGTATGGATTTCAGGGCTTCTACCTGGAGAAGGAAGTTGTGAAGGATTGGGA

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## FIGURE 2BB

TGACTTCTGCTTCTAGATTCTATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT  
AGGTTTATGATATAGACTTGTAATTCATGTTTTTTTATAACCTTGAAAATCATTCTAATG  
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG  
TGTTTAAGTTCTCTATTTTTTGTGTTTGTGTTTGTGTTGTAAGTTTTTGAGACAGGATCTC  
ACCATGTAACTTTGGCTGGCCTGGAACCAACTATGTAGACCAGGTAGACCTTAAACTGA  
CAGATCTGCCTGCGCTTGCCTCCCAAGCATTAGGACTGATGGTGTGTGTGACCATGCCCA  
GTTCTTCCTGGTTTTGTGTGTAGGTTTCTTCCCCTGACTTGGTACATGTGACATGTGA  
CAGATGTATGGAGTCTATAGAAGTGCCAGCAAAAATGGCCAGAATATTTATTTATTTT  
CTTAAAAATTTCCAAATTAAAGCTACTTAGTTAACAGTTAAACTGGCCAGGACTATATG  
AGATAAACTTGGTTTTCTATTTCTTTTTGT

SEQ ID NO: 38\_AA785735\_H

GGCAGGAGGCGCGCTGGCTGGGCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA  
GCAAGCGGAGCGCAGTTCGCCCCAAGCCAAGCCGCGCTGCCAACCTCCCGCCCCGCGCG  
CTCCTGTCCGCGGTGTCTAGCAGCGGGGCCAGCATGGTCATGGCGGATGGCCCGAGGCA  
CTTGACGCGCGGCGGTCCGGGTGGGGTTCTACGACATCGAGGGCACGCTGGGCAAGGG  
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA  
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA  
AATAATGAAAATGTTAGACCACCTCACATAATCAAACCTTATCAGGTAATGGAGACCAA  
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAAATTTTACTATCTTGC  
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATCTGGCAAATCCTGTCTGC  
TGTTGATTATTGTCTGCTGGTGGGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT  
GCTGGATAACAACATGAATATCAAAATAGCAGATTTTCGGTTTTGGAAAATTTCTTTAAAG  
TGTTGAAGTCTGGCAACATGGTGTGGCAGCCCCCTTATGCAGCCCCAGAAGTCTTTGA  
AGGCGAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT  
CCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT  
TCTGGAAGGAAGATTCCGGATTCCGTATTTTCATGTGAGAAGATTGCGAGCACCTTATCCG  
AAGGATGTTGGTCTTAGACCCATCCAAACGGCTAACCATAGCCCAAATCAAGGAGCATAA  
ATGGATGCTCATAGAAGTTCCTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA  
TGAGCCATCCATCGGGAGTTTAAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAAT  
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAAAGAGCTATAACCACTTTGCTGCCAT  
TTATTTCTTGTGTTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCAGTGAGCAGAG  
ACTTGATGGCCCGCCAGCGTCGGCCTAGCACCATTTGCTGAGCAAACAGTTGCCAAGGCACA  
GACTGTGGGGCTCCCAAGTGACCATGCATTACCGAACATGAGGCTGCTGCGATCTGCCCT  
CCTCCCCCAGGCATCCAACGTGGAGGCCCTTTTCAATTTCCAGCATCTGGCTGTGAGCGGA  
AGCTGCATTCTAGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA  
CCCTGTGCCTCCTGTCTGTGGTGGGAAGGGATGCCAGTCACTGCCCAGCAACATGATGGA  
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGGCCGAGGAAGACCCCGCTCATGC  
CTTTGAGGCATTTAGTCCACACGCGGGCAGAGACGGCACACTCTGTGAGAAGTGAC  
CAATCAACTGGTCTGTATGCCTGGGGCAGGGAAAATTTTCTCCATGAATGACAGCCCCCTC  
CCTTGACAGTGTGGAATCTGAGTATGATATGGGGTCTGTTTCAAGGGACCTGAACTTTCT  
GGAAGACAACCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTACCCCCGATGAC  
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCAGAA  
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAAGAGGGGCCGAGAGCATCAGATAC  
CTCCCTCACCAGGGAATTGTAGCATTTAGACAACATCTTCAGAATCTGGCTAGAACCAA  
AGGAATTCTAGAGTTGAACAAAGTGCAATTGTTGTATGAACAAATAGGACCGGAGGCAGA  
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA  
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCT  
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCCAGCCT  
TCTGTCAAAGGCCCAGAACACCTGTGAGCTTTATTGCAAAGAACCACCGCGGAGCCTTGA

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## FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA  
ACTGCAGGCCCTATTTTAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA  
GCAGCTGCCCCCTCCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTCAG  
CCTGACCCAGCCCCCTGAGCCCCCTCCTGGAGCCTTCCCTCCGAGCAGATGCAATACAGCCC  
TTTCCTCAGCCAGTACCAAGAGATGCAGCTTACAGCCCCCTGCCCTCCACTTCCGGTCCCCG  
GGCTGCTCCTCCTCTGCCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC  
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG  
TGAGCTGCCAAGCGCTGCTTCCCCCTGCGCCAGACTATCCCACTCCCTGT CAGTATCCTGT  
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCAGAAGCCCAGGACTGCA  
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG  
TGAAATGCTAGACGCTGTGGATCCACAACACACGGGTATGTCTGGTGAATTAGTCTCA  
GCACAGGAATTGAGGTGGGT CAGGTGAAGGAAGTGTATGTTCTTATTTTATTCAGC  
CTTTTAAATTTAAAGCTTATTTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC  
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGTAGGCTGAGGCAGGAGAATGGCGT  
CAAAGTTTTCTGTGGCAAGTGTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGT  
AACCCGGGAGGCGGAGCTTGCACTGAGCCAAAGATCGTGCCACTGCACTCCAGCCTGGCG  
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC  
TGTTTCTAAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT  
TCTACAGTGTGGTCTGAAGCACCTGTAATGTCAGAGCCCTTGTCTGGCCCTTGGTGCGAG  
GTGAACGAAAGCAGTGGAGCCTCTACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA  
TTTTTGTCTTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC  
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC  
ACTGGGGCAGATAGAGAACCAGGCGGCAGCAGTGTCTCGCAGACCCACCCAGGGAGAGC  
TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCACCCACAAGGGAGCAATAGCTTATAT  
TTGTACATTAGTTTTACCAAGCACTTTCTCTTCTAACCCTCACAACAATTCTATGAAATT  
AGCTGGGGAGATACTGTCTTATTTTTTTCAGCTGAAGAAACCAAGCTTTGGGAAGTTT  
GTGACTTCTCTGAGATCAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTGAC  
TGGCTTCTGGTTTTGGTTCTCTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTCCCTTCT  
CTTTCCTCAGTAGCATCTGACTCTTTTATAAGCAAACAGCTGTATAAACAAGCCCCCA  
TTTTGGTCAAGCACAGGGTGAATGTGATATTGTTCCCAACCTTATTCTCCACTCAACA  
GCCGCTGGCTTTGGGAAGAGGCGCCTTCAGGTGACAGTGCAGCTGTCCAGGTGGCCG  
TGCACTGAACCAGGCTGAGGGAGACAAAACCCCGCAGACCCGCTGCCTTTCAGCGTCC  
AGTTAACTGCAGAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC  
AGCAGTTTCTTACAGAACACCCCTTCCCTCAATTGCCAAGGGCGCATCGCACGGCATC  
AGGCCACCACTGCAGGCCAGCAGATTCCACCCAGGAACGGTCATGAAGTCAAGCTTTGT  
CTCAACGAGGGGCGTAACATTTCTTACAGTCAAGGCCCATCAACTAGAAGTGCTTATTA  
CTTTTAGGATTAAAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTCAGAGGCA  
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT  
ATGACCCAGATGGAATAATGTCACATTTCCCAAGTGCAGATAATGGGCTGCTGCTGGCTC  
TGTGGTGTCTGTCTGCAGAAGATTTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTC  
CACCATGGGTGGTAAGAGAAACCTGCCTTCACCAAAATCTCTGAAGGGGAAAGAAGTGGA  
GAGAAAGGTTTGCTTCACTTCGGGGACTGCAGTTTGAGAAATAAAGGGATACAGAGATA  
TCTGCACTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT  
TGCTGGATGTTTGGTCTGAAAGAGTTACTTTTGATAAAGTTAATCTAATTGTAGTTATAT  
TTTCTGTGTGCTTTTTTTTAACTAAGAAAAAATGGTGAGTTCAAGTACCTTTGGTA  
TTATGAGTGCAAATCATAAGCTCCAATGTGAAAAAATAATCAAAAGTATAACTTGTC  
ACTTAATGTTAGAAAATGCCTAAAATGCAGTGAATAAATAATCTCTGTACCAAATAGT  
AATTTAAATGGGGTAATTTTCTGCAAGGAAAATGTACTGTTTTTATGTTTCCAACCTCT  
TGA

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# FIGURE 2DD

SEQ ID NO: 39\_AA207220\_H

GCTGTGGCTCCCCGTCCTGGTGCGGGACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC  
 CTATTGATTCCCCTGCCGCCCTTGCTCCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTTC  
 GCGCGGCGCTCCGGCCCCACTCCCTCGGCCGAGAGCTAGCCCGGCCGCTGGCGGAAGGG  
 CTGATCAAGTCGCCCCAAGCCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG  
 CACAACCTGCGGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCACCTACGGGAAG  
 GTGAAGAAGGCGCGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC  
 AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTTCATCA  
 CTCAACCACCCTCACATCATTGCCATCCATGAAGTGTGAGAACAGCAGCAAGATCGTG  
 ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG  
 CTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGC  
 CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGATGCCAAT  
 GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG  
 CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC  
 ACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGC  
 ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC  
 TACCGGGAGCCACCTAAACCCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG  
 GTGAACCCACCCGCGCGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG  
 GGCTACGCCACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGT  
 GACTCTGCCCCGCGCTCCATGGCTGACTGGCTCCGGCGTTTCTCCCGCCCCCTCCTGGAG  
 AATGGGGCCAAGGTGTGAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACC  
 CCTGGCCTGGAGCGCCAGCATTTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCCAG  
 TCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAG  
 CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTGAGCCTCTGCAGAAGGGGTACAGGAGGAC  
 CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCCAGGCGAGGCTGCCCCCTGCTCCCCAAG  
 AAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGGCTACTACTCCTCTCCCGAGCCCC  
 AGTGAATCTGGGGAGCTCTTGAGCGCAGGCGACGTGTTTGTGAGTGGGGATCCCAAGGAG  
 CAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACCTCAAT  
 GGCAAGTTCTCCAGACAGCCTTGAGGCTCGCGGCCCCCACCACCTTCGGCTCCTTGGAT  
 GAACTCGCCCCACCTCGCCCCCTGGCCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG  
 GACAGCATCCTGTCTCTGAGTCTTTGACCAGCTGGACTTGCCCTGAACGGCTCCCAGAG  
 CCCCCACTGCGGGGCTGTGTGTCTGTGGACAACTCACGGGGCTTGAGGAGCCCCCTCA  
 GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTT  
 TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCA  
 AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCCGGTGAGGCTCTCAGATGCAGCTGG  
 TTGCACCCCGAGGGGAGATGCCTTCTCCCCACCTCCAGGACCTGCATCCAGCTCAGA  
 AGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG  
 AAATGCGCCAAGGGTTAGTGTCTGTCTTACGCCCTGCTGAACGAAGAGGATACTAAAGA  
 GAGGGGAACGGGAATGCCCGCGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGAGG  
 GGCCACAGAGA

SEQ ID NO: 40\_AA426580\_H, MAK\_V\_H

ATGCCGGCGGCGGGGACGGGCTCCTGGGGGAGCCGGCGGCGCCTGGGGGCGGCGGG  
 GGCGCGGAGGACGCGGCCAGGCCCCGCGGCGGCCTGCGAGGGAAGTTTCTGCTGCTGCTGG  
 GTGAGCGGCGTGCCCCGCGAGCGGCTCCGCGACTTCCAGCACCACAAGCGCGTGGGCAAC  
 TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGCTCCTTTGCCAAGGTGCGCGAGGGGCTG  
 CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGAGCCAAAAAG  
 GACACCTATGTCACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC  
 CCCAATATCACTCAGCTCCTTGATATTTAGAAAACGGAAAACAGCTACTACCTGGTCTATG  
 GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

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## FIGURE 2EE

TCCGAAGCCCGCAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGCC  
GGGGTGGTCCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC  
AAGCTGATTGACTTTTGGTTTGAAGCAACTGCGCAGGGATCCTGGGTACTCGGATCCGTTT  
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAG  
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG  
CTGCCTTTTACGGTGGAGCCTTTTACGCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA  
GAAATGAACCCCTCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCTGCGCTCTCTC  
CTGGAACCGGATCCTGTGAAGAGGCCAAAATTTAGCAGGCACTGGCGAATCGCTGGCTT  
AATGAGAATTACACGGGCAAAGTGCCTGTAAATGTACCTATCCCAACAGGATTTCTCTG  
GAAGATCTGAGCCCGAGCGTCTGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC  
GACGTGATCAACACTGTGCTCTCAACCGCGCTGCCACATCCTGGCCATCTACTTCCTC  
TTAAACAAGAACTGGAGCGCTATTTGTGAGGAAATCTGACATCCAGGACAGCCTCTGC  
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGGAGTCTATGAGGCC  
TCTCTGGACACCTGGACACGAGATCTTGAATTCATGCCGTGCAGGATAAAAAGCCCCAA  
GAAACAAGAAAAAGAGGGGATTTTCTTATCGACCATCTCCAAGAAGTTGGACAAGAAC  
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTCAGAACACCAAGCC  
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCTTTGGCTGC  
CGCAATATTTTCCGCAAAACCTCAGATTCCAATTGTGTGGCTTCTTCTTCCATGGAGTTC  
ATCCCCGTGCCACCGCCAGGACCCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA  
GGGCCCCGAAGCACTGGCATCCCCCAAGGAAGACCCCTGATGCTGGACATGGTGGCG  
TCCTTCGAGTCTGTGGATCGCGACGACCAGTAGAAGTGTGTCTCCTCTCATCACTAC  
AGGATTCTGAACTCCCCGGTCTGCTTGGCTCGCAGAAATTCAGCGAGAGGACGCTGTCC  
CCGGGTCTGCCATCCGGAAGCATGTGCGCTCTCCATACTCCTTTGCTCCAATCTGGTC  
TCTTTTGCTCAGGAAGATAAGAACAGCCCCCAAAAGAGGAGGGCCTGTGTTGCCACCT  
CCGGTCCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA  
GGCCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG  
CCATCTGCAGATAGGCCCTGGAGGCCAGCCTGCCCCCACTGCAGCCCCTAGCCCCTGTG  
AACCTTGCTTTGACATGGCCGATGGGGTCAAGACCCAGTGCTAA

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ATGGACACAAAGCTGAACATGCTGAACGAGAAGGTGGACCAGCTCCTGCACTTCCAAGAA  
GATGTACAGAGAAGTTGCAGAGCATGTGCCGAGACATGGGCCACCTGGAGCGGGGCTG  
CACAGGCTGGAGGCCTCCCGGGCACCGGGCCGGGGCTGATGGGGTTCCCCACATT  
GACACCCAGGCTGGGTGGCCCGAGGTCTTGGAGCTGGTGAGGGCCATGCAGCAGGATGCG  
GCCCAGCACGGTGGCAGGCTGGAGGCCCTCTTCAAGATGGTGGCTGCGGTGGACAGGGCC  
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCTCATGCAGGGG  
CGTGTGCCCTGGAGGAGAGGCAGCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG  
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGACAGGACAGAGCCTGCAG  
AAGGATAAGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG  
ATCATGGTGACAGCGGCAAATAAAGAGCGAGTGGAGAAGAGGGAGGAAAACCAAGCAT  
GTGCTGAGCACCAGTGGGGTGCACTCTGATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG  
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCATCAGAGCGTCAGGGCTGGGA  
GCTGACCCCGCCAGGCAGTGGTCTACCGGGCCAGGGAGATGGTGTTCCTGGCCAGCC  
CAGGCATTCCCTGGCCACCTGCCCCCTGCCCAAAAGGTGGAAGCCAAGGCTCCTGAGACA  
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACCCGGCAGGGTCAATGTG  
GTCTCCCCGAGCCTGGAGGTTGCACAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT  
GACCTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGGCCA  
GGCCCTCAGGGCTGCCAGCCAGGGCAACCCACAGTGGTGGAGAAACACCTCCA  
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGT  
CCTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATACAAGAGATGGATACTCCT

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FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGAGCCTTGGACCCACCCTCACCACAGAGGCTCCA  
GCAGCTGCCCAGCCAGGCAAGCAGGGGCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCT  
GGGACTGAGCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCGCTGCAGGAG  
AGCAGCAGCCCCGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGGTGGGGCCGAGCCTGGC  
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG  
CAGCAGGGCAAAGCCCCAGGGGCGGGAAACCCTGAGCCTGAGCAGGACTGTGCAGCCAGG  
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCCAGGCGCGGAGGCTGGCAGCGTG  
GTTCTGGATGACAGTCCGGCCCCCAGGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG  
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGTTCGG  
TTTGGCCAGGTCCACAGGTGCACAGAGAAGTCCACAGGCCTCCCACTGGCTGCCAAGATC  
ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC  
CAGCTCAGCCACGTGAACCTGATCCAGCTCTATGACGCCTTCGAGAGCAAGCACAGCTGC  
ACCTTGTCTATGGAGTACGTGGACGGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG  
TACCACCTGACTGAGCTGGATGTGGTCTGTTCACCAGGCAGATCTGTGAGGGTGTGCAT  
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC  
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT  
CGAGAGAAGCTGAAGGTGAACCTTCGGCACTCCTGAGTTCTTGGCCCCAGAAGTCGTCAAT  
TATGAGTTTGTCTCATTCCCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA  
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTTATTGTA  
AACTGTAGCTGGGATTTTGATGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC  
TTTGTTCCTCCGGTTGCTGGTCAAAGAGAAGAGCTGCAGAAATGAGTGCCACACAGTGCCTG  
AAACACGAGTGGCTGAATAATTTGCCTGCCAAAGCTTCAAGATCCAAAACCTCGTCTCAAA  
TCCCAACTACTGCTGCAGAAATACATAGCTCAAAGAAAATGGAAGAAACATTTCTATGTG  
GTGACTGCTGCCAACAGGTTAAGGAAATTTCCAACCTTCTCCCTAA

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GGGGAGATGGCGCTGTTTGAGTGCCTGGTGGCGGGGCCCACTGACGTGGAGGTGGATTGG  
CTGTGCCGTGGCCGCTGCTGCAGCCTGCACTGCTCAAATGCAAGATGCATTTTCGATGGC  
CGCAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGGCGTCTACACCTGC  
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGCCCGGCTGACCGTGCGGCCCTCG  
TTGGCACCCCTGTTTACACGGCTGCTGGAAGATGTGGAGGTGTGGAGGGCCGAGCTGCC  
CGTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGAATCATTGTCG  
TGCCCCATGGAGGAGAGTGAGAACTTGCGGCTGCGGCAGGACGGGGGTCTGCACTCACTG  
CACATTGCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTCACTGCTGTTAACACC  
CATGGCCAGGCCCACTGCTCAGCCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCTCA  
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCCGAGGAGCCAGAGCAGGGTGAG  
CTGGAGCGGCTGTCCATTCCCGACTTCTGCGGCCACTGCAGGACCTGGAGGTGGGACTG  
GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCTGCCCTACCCACCATCAGCTGG  
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT  
GTCCATCGCTTGGTGTTCCTGCGGTGGGGCCTCAGCACGCCGCTGTCTACAAGAGCGTC  
ATTGCCAACAAGCTGGGCAAAGCTGCCTGCTATGCCCACCTGTATGTACAGATGTGGTC  
CCAGGCCCTCCAGATGGCGCCCCGAGGTGGTGGCTGTGACGGGGAGGATGGTCACACTC  
ACATGGAACCCCCCAGGAGTCTGGACATGGCCATCGACCCGGAATCCCTGACGTACACA  
GTGCAGCACCAGGTGCTGGGCTCGGACAGTGGACGGCACTGGTACAGGCCTGCGGGAG  
CCAGGGTGGGCAGCCACAGGGCTGCGTAAGGGGGTCCAGCACATCTTCCGGGTCCCTCAGC  
ACCACTGTCAAGAGCAGCAGCAAGCCCTCACCCCTTCTGAGCCTGTGCAGCTGCTGAG  
CACGGCCCAACCCTGGAGGAGGCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG  
GTGGAGGGACAGCCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGCCAGGTGCTC  
TGGAGGAGCTGCCGAGGGGCCCTCTAGAGGCACGGGCGGTGTGTACGAGCTGAGCCAG  
CCAGATGATGACCAGTACTGTCTCGGATCTGCCGGGTGAGCCGCGGGACATGGGGGCC

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## FIGURE 2GG

CTCACCTGCACCGCCCCGAAACCGTCAACGGCACACAGACCTGCTCGGTACATTGGAGCTG  
GCAGAGGCCCCCTCGTTTGTAGTCCATCATGGAGGACGTGGAGGTGGGGGCTGGGGAACT  
GCTCGCTTTGCGGTGGTGGTTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC  
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGCTCC  
CTGGTGGTGTCTCAGCACGGGGGCCAGGATGGAGGCGTCTACACCTGCACCGCCCAGAAC  
CTGGCGGGTGAGGTCTCCTGCAAAGCAGAGTTGGCTGTGCATTGAGCTCAGACAGCTATG  
GAGGTGAGGGGGTTCGGGGAGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTTTAT  
GACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCCTACTTGCGGCGCATAGTGGAGCGT  
AGCTCCGGCCTGGAGTTTTCGGGCCAAGTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA  
GCGCGTTCGGGAGGCCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCTCTACTTCCAT  
GAGGCCTTCGAGAGGCGCCGGGACTGGTTCATTGTGTCACCGAGCTCTGCACAGAGGAGCTG  
CTGGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCCTATATGCGG  
CAGGTGCTAGAGGGAATACTACCTGCACAGAGCCACGTGCTGCACCTCGATGTCAAG  
CCTGAGAACCTGTGGTGTGGGATGGTGTGCTGCGGGCAGCAGCAGGTGCGGATCTGTGAC  
TTTGGGAATGCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGGCACACCT  
GAGTTTGTAGACCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG  
CCTGTGGGTGTTGTTGCCTTCTCTGTCTGACAGGAATCTCCCCGTTTGTGGGGAAAT  
GACCGACAACATTGATGAACATCCGAAACTACAACGTGGCCTTCGAGGAGACCATTTC  
CTGAGCCTGAGCAGGGAGGCCCCGGGGCTTCTCATCAAAGTGTGGTGACGAGCCGGCTG  
AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGGTTCAAACTCAGGCAAGGGCGCA  
GAGGTGAGCACGGATCACCTGAAGCTATTCTCTCCCGCGGAGGTGGCAGCGCTCCCAG  
ATCAGCTACAAATGCCACCTGGTGTGCTGCGCCCCATCCCCGAGCTGCTGCGGGCCCCCA  
GAGCGGGTGTGGGTGACCATGCCCCAGAAGGCCACCCCCAGTGGGGGGCTCTCATCTCC  
TCGGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCACTGCAGCCC  
GAGTTCTCTGGCTCCCGGTGTCCCTCACAGACATTCCCACTGAGGATGAGGCCCTGGGG  
ACCCAGAGACTGGGGCTGCCACCCCCATGGACTGGCAGGAGCAGGGAAGGGCTCCCTCT  
CAGGACCAGGAGGCTCCAGCCCCAGAGGCCCTCCCTCCCCAGGCCAGGAGCCCGCAGCT  
GGGGCTAGCCCCAGGCGGGGAGGCTCCGCAGGGGCAGCTCGGCTGAGAGCGCCCTGCC  
CGGGCCGGGCGCGGGAGCTGGGCGGGGCTGCACAAGGCGGCGTCTGTGGAGCTGCCG  
CAGCGCCGAGCCCCGGGAGCCACCCGCTGGCCCCGGGGAGGCCCCGAGGAT  
GAGTATGCCCAGAGGCTGCAGGCCCTGCGCCAGCGGCTGCTGCGGGGCGGTGCTCGGGAC  
GGCAAGGTGAGCGGCTCAGGGGTCCCTGCTGGAGAGCCTGGGGGCGGTGCTCGGGAC  
CCCCGATGGCAGGCTGCCTCCAGCGAGGCGCGCCCCACACAGCCCCACTCGAG  
AACCGGGCCTGCAAAAGAGCAGCAGCTTCTCCAGGGTGAGGCGGAGCCCCGGGGCCGG  
CACCGCCGAGCGGGGCGCCCTCGAGATCCCCGTGGCCAGGCTTGGGGCCCGTAGGCTA  
CAGGAGTCTCCTTCCCTGTCTGCCCTCAGCGAGGCCAGCCATCCAGCCCTGCACGGCCC  
AGCGCCCCCAAACCCAGTACCCCTAAGTCTGCAGAACCTTCTGCCACCACACCTAGTGAT  
GCTCCGCAGCCCCCGCACCCAGCCTGCCCAAGACAAGGCTCCAGAGCCCAGGCCAGAA  
CCAGTCCGAGCCTCCAAGCCTGCACACCCCCCAGGCCCTGCAAACCTAGCGCTGCCC  
CTCACACCTATGCTCAGATCATTCAGTCCCTCCAGCTGTGAGGCCACGCCAGGGCCCC  
TCGCAGGGCCCTGCCGCGCCGCTTCAGAGCCCAAGCCCCACGCTGCTGTCTTTGCCAGG  
GTGGCCTCCCCACCTCCGGGAGCCCCCGAGAAGCGCGTGCCTCAGCCGGGGTCCCCCG  
GTGCTAGCCGAGAAAGCCCCGAGTTCACCGGTGCCCGCCAGGCCAAGTTCAAGCGCAGCCG  
AGCAGCATCGAAAACCTTGAGTCGGAGGCGGTGTTTCGAGGCCAAGTTCAAGCGCAGCCG  
GAGTCGCCCCCTGTGCTGGGGTGGGCTGCTGAGCCGTTTCGCGCTCGGAGGAGCGCGG  
CCCTTCGTTGGGGCCGAGGAGGAGGATGGCATATACCGGCCAGCCCGCGGGGACCCCC  
CTGGAGCTGGTGGCAGCGCCTGAGCGCTCACGCTCGGTGCAGGACCTCAGGGCTGTGCGA  
GAGCCTGGCCTCGTCCGCGCCTCTCGCTGTCACTGTCCAGCGGCTGCGGCGGACCCCT  
CCCGCGCAGCGCCACCCGGCCTGGGAGGCCCGCGGGGACGGAGAGAGCTCGGAGGGC  
GGGAGCTCGGCGGGGCTCCCCGGTGTGGCGATGCGCAGGCGGCTGAGCTTCAACCTG

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## FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGGCGCGTCC  
GGCCGCAGCACGCCGCTGTTTCGGACGGCTTCGACGGGCCACGTCCGAGGGCGAGAGTCTG  
CGGCGCCTTGCCCTTCCGCACAACCAAGTTGGCCGCCAGGCCGGCCACCACGCCTTCC  
GCCGAGTCCCTGGGCTCCGAGGCCAGCGCCACGTCCGGGCTCCTCAGCCCCAGGGGAAAGC  
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTATCGCCACCA  
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTACCAGTACGTGCGCAGTGAGTCAGAC  
TTCCCCCAGTCTTCCACATCAAACCTCAAGGACCAGGTGCTGCTGGAGGGGAGGCAGCC  
ACCCTGCTCTGCCCTGCCAGCGGCCTGCCCTGCACCGCACATCTCCTGGATGAAAGACAAG  
AAGTCCTTGAGGTCAAGCCCTCAGTGATCATCGTGTCTCTGCAAAGATGGGCGGCAGCTG  
CTCAGCATCCCCCGGGCGGGCAAGCGGCACGCCGGTCTCTATGAGTGCTCGGCCACCAAC  
GTACTGGGCAGCATCACCAGCTCCTGTACCGTGGCTGTGGCCCCAGTCCCAGGAAAGCTA  
GCTCCTCCAGAGGTAACCCAGACCTACCAGGACACGGCGCTGGTGCTGTGGAGCCGGGA  
GACAGCCGGGCACCTTGACGTATACGCTGGAGCGGCGAGTGATGGGGAGTCTGTGTGG  
CACCCTGTGAGCTCAGGCATCCCCGACTGTTACTACAACGTGACCCACCTGCCAGTTGGC  
GTGACTGTGAGGTTCCGTGTGGCCTGTGCCAACCGTGCTGGGCAGGGGCCCTTCAGCAAC  
TCTTCTGAGAAGGTTCTTGTGAGGGTACTCAAGATTCTTCAGCTGTGCCATCTGTCTGCC  
CACCAAGAGGGCCCTGTACCTCAAGGCCAGCCAGGGCCCCGGCCTCCTGACTCTCCTACC  
TCACTGGCCCCACCCCTAGCTCCTGTGCTGCCCCACACCCCCGTGAGTCACTGTGAGCCCC  
TCATCTCCCCCACACCTCCTAGCCAGGCCTTGTCTCGCTCAAGGCTGTGGGTCCACCA  
CCCCAAACCCCTCCACGAAGACACAGGGGCTGCAGGCTGCCCCGCCAGCGGAGCCACC  
CTACCCAGTACCCACGTACCCCCAAGTGAGCCCAAGCCTTTCTGCTCTTGACACTGGGACC  
CCGATCCCAGCCTCCACTCCTCAAGGGGTTAAACCAGTGTCTTCTCTACTCCTGTGTAT  
GTGGTGACTTCTTTGTGTCTGCACCACAGCCCTGAGCCCCAGCCCTGAGCCCCCT  
CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCCGCCAAGGAGGTGGTCACTCC  
CCTGGGAGCAGTCCCCGAAGCTCTCCAGGCCTGAGGGTACCACTCTTCGACAGGGTCCC  
CCTCAGAAACCCCTACACCTTCTGGAGGAGAAAGCCAGGGGCGCTTTGGTGTTGTGCGA  
GCGTGCCGGGAGAATGCCACGGGGCGAACGTTCTGGGCCAAGATCGTGCCCTATGCTGCC  
GAGGGCAAGCCGCGGGTCTGCAGGAGTACAGAGGTGCTGCGGACCCTGCACCACGAGCGG  
ATCATGTCCCTGCACGAGGCCTACATACCCCTCGGTACCTCGTGCTCATTGCTGAGAGC  
TGTTGGCAACCGGGAACCTCTGTGGGCTCAGTGACAGGTTCCGGTATTCTGAGGATGAC  
GTGGCCACTTACATGGTGCAGCTGCTACAAGGCCTGGACTACCTCCACGGCCACCACGTG  
CTCCACCTAGACATCAAGCCAGACAACCTGCTGCTGGCCCCCTGACAATGCCCTCAAGATT  
GTGGACTTTGGCAGTGCCCAGCCCTACAACCCCCAGGCCCTTAGGCCCTTGGCCACCGC  
ACGGGCACGCTGGAGTTCATGGCTCCGGAGATGGTGAAGGGAGAACCCATCGGCTCTGCC  
ACGGACATCTGGGGAGCGGGTGTGCTCACTTACATTATGCTCAGTGGACGCTCCCCGTTT  
TATGAGCCAGACCCCCAGGAAACGGAGGCTCGGATTGTGGGGGGCGCTTTGATGCCTTC  
CAGCTGTACCCCAATACATCCCAGAGCGCCACCCTCTTCTTGCGAAAGGTTCTCTGTGA  
CATCCCTGGAGCCGGCCCTCCCTGCAGGACTGCCTGGCCCCACCCATGGTTGCAGGACGCC  
TACCTGATGAAGCTGCGCCGCCAGACGCTCACCTTCACCACCAACCGGCTCAAGGAGTTC  
CTGGGCGAGCAGCGGCGGGCGGGCTGAGGCTGCCACCCGCCACAAGGTGCTGTGCGC  
TCCTACCCCTGGCGGCCCCCTAGAGGCACGGACCACAGCCAGGCCTCGGGCTTCAACTGGGG  
TTCCCACCAATGCCACGGGACATTCCAGGGGCCACGCTGAGCCAGGCGGGCTGGGGCTT  
CGGTTACCACCAGCAGCAACATCTGGCTGGGCTCTTACCTCATAGACCTTCAAGGACAGA  
GACCCAGGGCCTGGACCTGATGCCACCCAGGCCAAAGCCAGAGTGGGAGACCCATTGG  
TCAGGCTCAGCAGGTTGGGAACAGGCAGAGGGACAAGAGGGGAATGGAGAAGTGAGAGG  
AAAAGGAATCGAGGGACAGGAAGGGGGAGGCTCTAGGAAGGTTCTGGGTTGGGGGTGAGT  
GCATCTCAGGGAGAACCAAGGAAGGTGGGCATGGCTGGAGAGGAGGAAAAGGAAGGAGCC  
CCAGGTGTGAGGGCAGTAGGCTGGGAGTCAGTGTGGCAAAGCGGGGGCAGGACACAGATA  
CAGTGGCAGGGGGCCAGGGCTGGGACATGAGAGAAGGCAGCGAGGCGGCAGAGGGAGAAG  
AGAGGACTCAGGTGGAGGTGGGGTGGGTGAGCTGTGAGCATCCCTCAGAGGAGAAATGTG

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## FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCCTCCTGTCCAGTGGATACAGC  
CCTGGGCGCTCTGCTGGCCCAAGGATGTCCCCACTGCCCCCTCCATGGCCTTTGGCCTTCT  
TCCCATTTCATATTTATTTATTTATTTACTTTTATGAAGTTTCCCCTTCCATCCGATCCCT  
ACTGCCCATGTTGTCCTGACCATCCCTCCCAGCCATCCAGCTGTCTGTCTGTCTGCCACA  
AGGAAATAAAAATGGCAAGCAGCAAAAAA

SEQ ID NO: 43\_AA542015\_M SGK088\_M  
GCCACGGACATCTGGGGAGCGGGTGTGCTCACCTACATCATGCTTAGTGGGTACTCCCCA  
TTCTATGAGCCAGACCCCCAGGAAACAGAGGCTCGGATTGTTGGGGTTCGCTTTGATGCC  
TTCCAGTTGTATCCTAACACATCCCAGAGTGCCACCCTCTTCTTGAGAAAGGTCCTCTCA  
GTACATCCCTGGAGCCGGCCCTCTCTGCAGGACTGCTTGGCCACCCATGGCTGCAAGAT  
GCCTACCTGATGAAGCTGCGCCGCCAGACACTCACCTTACCACCAACCGGCTCAAGGAA  
TTCCTGGGCGAGCAGCGCGACGTGGGCTGAGGCTGTACCCGTCAAGGTGCTGCTC  
CGCTCCTACCCTGGCAGCCCCCTAGGTGGCAGACCCGAGCCCGGCCACGGGCTTCAACT  
TGGGTTCTCACTCGCGCTGCCAAGGGACATTCCAGAGCCCATGCTGAGCTGGACAGGCAG  
GGGCTTCAGATACCAGCAGCAGCAGCAGCAGCAGCAACATCTGGCTGGGCTATT  
ACCTCATGGACCTAAGAGGACAAGGCCCTGGGGCTTCAGCCGAATGTACCCCGGCCATA  
ACCAGAGCAGGAGACCCACTGGCCAGGCTGGGCAAGGGTGAGAGCAGAAAGAGGCAAGA  
GGGAGTTGGGAAGTGAAGAATGAGACGGAGGATAGAGAGGGAGGAGTTTGAGGAAGGTTT  
TAGGCTGGAGTGAATGCTATATCTCAGGGAGAAGCCAGAAGGGGACATGGCTGAAGAGG  
AAGAAGGACCCTGTGATGTGGGAATGTGGTGGAGAGGAGGACTGGACATAGAGAGTGTGC  
CAGGAGCCAGAGCAGAGACATAAAGGGAGGGCAGAAGGGTAGAAGGCAACAGGAGTGGGCT  
CAGGGGTGGCAGGGCAGGCCAGCAGCTGCATCTTCAGAAAGAGAGAGGAGAAAGGCAAG  
AGACGAAAGGCCGCTCCAGCTGGTCTCCTGTCCCAGCCGATGCAGTTCTGGGCGTTCTCC  
ACTGGCCAGGGATGTCTCTCACTGCTCCTCCATGGCCTTTGCCCTCCTTCCATTGTAT  
TTATTTATTTATTGCCTTTTGTGGAGTTTCTTTCTATCCAGTCCCTAGTGCCTATGTTG  
TCCCGACCATCCCCCTTCAGTCACCCAGCTGTCTGTGCAGCTGTCTGTCTGTCTCACA  
AGGAAATAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAGC

SEQ ID NO: 44\_R19772\_H  
ATGAAGGGCGGCGACAGGGCTTACACCCGAGGTCCCTCTTTGGGGTGGCTCTTTGCTAAG  
TGCTGCTGTTGCTTCCCCTGTAGAGATGCATACTCTCATTCCTCAAGCGAGAATGGAGGC  
AAGTCCGAGTCCGTAGCCAACCTGCAGGCCAGCCCTCCCTGAACTTCATCCACAGTTCC  
CCGGGTCCCCAAGCGCTCCACCAACACTCTTAAGAAGTGGCTGACGAGTCTGTGCGTCGG  
CTCAACAGCGGGAAGGCAGATGGAAACATCAAAAAGCAGAAGAAAGTTCCGCGATGGTCGG  
AAGAGCTTTGACCTGGGATCTCCCAAGCCTGGGGATGAAACAACCCCTCAGGGAGACAGC  
GCTGATGAGAGCAAGAAAGGTTGGGGTGAAGATGAGCCGGATGAAGAGTCAACACACCC  
CTCCCACCACCTATGAAGATTTTGTACAACGACCCTACACAGGATGAAATGTCTCTCTCT  
TTGCTAGCAGCCCGGCAGGCTTCCACTGAAGTACCTACTGCTGCAGACCTTGTCAATGCA  
ATAGAAAAGTTGGTCAAAAACAAGCTGAGTCTAGAAGGAAGCTCATAACCGGGGGAGCTTG  
AAAGACCCTGCAGGCTGCCTGAATGAGGGGATGGCCCCACCCACACCTCCTAAAAATCCA  
GAAGAAGAACAGAAAGCCAAGGCCCTGAGAGGCAGGATGTTTGTCTGAATGAGCTGGTA  
CAGACAGAGAAAGACTATGTCAAGGATCTGGGCATTGTGGTGGAGGGCTTCATGAAGAGA  
ATAGAAGAAAAGGGTGTCCCTGAGGATATGCGAGGAAAGGACAAAATCGTGTGTTGAAAT  
ATTCATCAGATTTATGACTGGCATAAGGATTTTTCCTGGCGGAACTGGAAAAGTGTATC  
CAGGAGCAAGACAGATTGGCACAGCTCTTTATTAAGCACGAGCGGAAGCTGCACATCTAC  
GTGTGGTATTGTGAGAATAAGCCGCGCTCAGAGTACATCGTTGCTGAGTATGACGCCTAC  
TTTGAGGAGGTAAAACAGGAGATAAATCAGAGGCTGACACTGAGTGACTTCTCATCAAG  
CCCATTGAGAGAATAACAAAATACCAGTTGCTCCTCAAGGACTTCTGAGATACAGTGAG  
AAGGCTGGTTTGGAGTGTTCAGATATCGAGAAAGCAGTGGAGTTAATGTGCCTTGTTC

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## FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT  
GCTCAGGGGAAGCTACTGCAGCAGGACACATTCTATGTGATCGAGCTGGATGCAGGCATG  
CAGTCCCGGACCAAAGAGAGGGCGGTGTTCTCTCGAGCAGATTGTTCATCTTCAGTGAA  
CTGCTCAGGAAGGGATCCCTCACCCCTGGCTACATGTTCAAAAGGAGCATCAAGATGAAT  
TACTTGGTCCTGGAGGAGAATGTGGACAATGATCCCTGCAAGTTTGCACATCAAGACAGA  
GAGACTTCTGAGAGGGTTGTTCTGCAAGCCGCCAACGCTGACATCCAGCAGGCCTGGGTG  
CAGGACATCAATCAAGTCTTAGAAACACAGCGAGACTTTTGAATGCACTGCAATCGCCC  
ATTGAGTATCAACGGAAAGAAAGGAGCACAGCTGTGATGAGGTCTCAACCTGCCAGGCTT  
CCCCAAGCCAGCCCCAGGCCCTACTCTCTGTTCTCTGCGGGCTCAGAGAAGCCCCCAAAG  
GGCTCCAGCTATAACCCACCTCTGCCTCCCTGAAGATATCTACCTCCAATGGCAGTCCA  
GGGTTTGAATACCACAGCCTGGGGACAAGTTCGAAGCCAGCAAGAACGACCTGGGAGGC  
TGCAATGGGACCTCGTCCATGGCCGTGATCAAAGATTACTATGCACTGAAGGAGAATGAA  
ATCTGTGTGAGCCAAGGTGAGGTGGTCCAGGTCTCGCCGTCAACCAGCAGAACATGTGT  
CTGGTGATACCAGCCTGCCAGCGACCATTTCCCCCGCCGCGAGGGCTGGGTCCCAGGCAGC  
ATCCTGGCGCCCCCTCACCAAAGCCACAGCAGCAGAAAGTAGTGACGGGAGCATCAAGAAG  
TCATGTTTATGGCATACTCTACGCATGAGAAAGCGGGCGGAAGTGGAGAACACGGGTAAA  
AATGAAGCCACAGGGCCTCGTAAACCCAAGGATATTCTGGGCAACAAAGTCTCTGTAA  
GAGACGAACAGTTCGGAGGAATCAGAGTGTGATGATCTTGACCCTAATACTAGCATGGAG  
ATCTTAAATCCAAATTTTATCCAAGAAGTGGCCCCAGAATTCCTTGTGCCCTTGGTGGAT  
GTGACCTGCTTGCTTGGGGACACAGTGATACTGCAGTGCAAAGTCTGTGGGCGGCCAAG  
CCCACCATCTTGGAAGGGTCCAGACCAGAACATCCTTGACACTGATAACAGCTCAGCC  
ACATACACGGTCTCCTCTTGTGATTCTGGAGAAATCACCTGAAGATCTGTAATCTGATG  
CCCCAAGACAGTGGGATTTATACCTGCATAGCAACAAATGACCACGGGACCATCAACG  
TCTGCAACAGTCAAAGTGCAAGGTGTTCCAGCAGCCCCCTAACCGCCCCATTGCCAGGAG  
AGAAGCTGCACCTCCGTGATTCTCCGCTGGCTGCCCCCTCCAGCACAGGAACTGCACT  
ATTTCTGGTTTACACTGTGGAGTACAGAGAGGAAGGTTCTCAGATCTGGCAGCAGTCAGTG  
GCTTCGACCTTGACACTTACCTCGTCATCGAAGACCTTAGTCCCGGGTGTCTTATCAG  
TTCAGAGTCAGTGCCAGTAACCCCTGGGGAATCAGCCTTCCAGCGAGCCCTCGGAGTTT  
GTGCGACTTCCAGAATACGATGCTGCTGCTGATGGTGCCACCATTCTTGAAGGAAAAAT  
TTGACTCAGCTTACACTGAGCTGAATGAAATTGGAAGAGGCCGTTTCTCTATAGTAAAG  
AAATGCATTACAAAGCTACCCGCAAAGATGTGGCTGTGAAATTTGTTAAACAAAAAATG  
AAGAAGAAAGAACAGGCTGCCCCAGGAGGTGCCCTGCTTACGACCTACAGCACCCCCAG  
TACATCACTCTCCATGACACCTATGAGTCCCCCACATCCTACATCCTGATCTTGAACTG  
ATGGATGATGGCCGGCTCTTAGACTACCTTATGAATCATGATGAACTGATGGAGGAAAA  
GTAGCTTTCTATATCCGAGACATCATGGAGGCTCTGCAGTACCTTCACTGACAGGGTT  
GCACATTTGGACATAAAGCCTGAAAACCTGCTCATTGACCTACGGATTCCAGTGCCTCGA  
GTGAAGCTCATTGACTTGGAGGATGCTGTCCAGATCTCGGGTCACTTCCACATTACCAC  
CTGCTGGGGAACCTGAGTTTGCTGCCCCAGAAGTCATTCAAGGCATCCCCGTCTCCCTG  
GGGACAGACATCTGGAGCATCGGGGTTCTGACATATGTATGCTGAGTGGGGTCTCCCC  
TTCTTGGATGAGAGCAAAGAGGAGACATGTATCAACGTATGCAGGGTGGATTTAGCTTC  
CCCCATGAATACTTCTGTGGTGTGAGCAATGCTGCCAGAGATTTATCAATGTGATCTTA  
CAGGAAGATTTTCGGAGGCGGCCACAGCAGCCACATGCTTGCAGCATCCATGGCTGCAG  
CCCCATAATGGCAGCTACTCTAAGATCCCCCTGGACACCTCCCGCCTAGCATGCTTCATA  
GAACGTCGCAAGCACCAAGATGATGTGCGGCCTATCCCCAATGTCAAGAGCTACATTGTC  
AACCGGGTGAACCAAGGGACGTAG

SEQ ID NO: 45\_5R72\_8\_2\_H  
CGCCGCTGTTTGTCTCGCGCGGCCCCGTCCACTGCCCTGCGGTTGCTCTGCGGGCTGAA  
AAGTTTCTCCCGGTGCAGAAATCCGGGCTCAGCGACAGCCTGCGCCGAGTGTGCGCACCT  
GTCCGAGACCCGCCAGTCCGCGCGCCCCGGCTTTGTTTCGTGCGGAAGTGTAGTGGTGAGA

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## FIGURE 2KK

AAAACTCCATGTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC  
TGGGCTGTACGTGTGAATATGTGTCTAGTGCATCCTTAACCTGAGGACTTCACCAAGTTC  
GAAATTACAGTTTTTACCATCACTACCTTATCCTTTTTGGCCTGGTTTTCTTCTCCTCAA  
CAGTGGAAACATTTTTAAAGTTGCTTTTGTGTCAGAGTTAAACAAATGGCTGATAGTGGC  
TTAGATAAAAAATCCACAAAATGCCCCGACTGTTTCTCATCTGCTTCTCAGAAAGATGTACTT  
TGTGTATGTTCCAGCAAAACAAGGTTTCCCTCCAGTTTGGTGGTGAAATGTACAGACA  
TCAAGCATTGGTAGTGCAGAACTTTAATTTCACTGGAGAGAAAAAAGAAAAAATATC  
AACAGAGATATAACCTCCAGGAAAGATTTGCCCTCAAGAACCTCAAATGTAGAGAGAAAA  
GCATCTCAGCAACAATGGGGTTCGGGGCACTTTACAGAAGGAAAAGTTCCCTCACATAAGG  
ATTGAGAATGGAGCTGCTATTGAGGAAATCTATACCTTTGGAAGAATATTGGGAAAAGGG  
AGCTTTGGAATAGTCATTGAAGCGACAGACAAGGAAACAGAAACGAAGTGGGCAATTAA  
AAAGTGAACAAAGAAAAGGCTGGAAGCTCTGCTGTGAAGTTACTTGAACGAGAGGTGAAC  
ATTCTGAAAAGTGTAACAATGAACACATCATACCTGGAACAAGTATTTGAAAACGCCA  
AAGAAAATGTACCTTGTGATGGAGCTTTGTGAGGATGGAGAACTCAAAGAAATTCTGGAT  
AGGAAAGGGCATTCTCAGAGAATGAGACAAGGTGGATCATTCAAAGTCTCGCATCAGCT  
ATAGCATATCTTCACAATAATGATATTGTACATAGAGATCTGAAACTGGAAAAATATAATG  
GTTAAAAGCAGTCTTATTGATGATAACAATGAAATAAACTTAAACATAAAGGTGACTGAT  
TTTGGCTTAGCGGTGAAGAAGCAAAGTAGGAGTGAAGCCATGCTGCAGGCCACATGTGGG  
ACTCCTATCTATATGGCCCCCTGAAGTTATCAGTGGCCACGACTATAGCCAGCAGTGTGAC  
ATTTGGAGCATAGGAGTCGTAATGTACATGTTATTACGTGGAGAACCACCCTTTTTGGCA  
AGCTCAGAAGCGAAGCTTTTTGAGTTAATAAGAAAAGGAGAACTACATTTTGAAAATGCA  
GTCTGGAATTCCATAAGTGAAGTGTGCTAAAAGTGTGTTTGAACAACCTTGAAGTAGAT  
CCTGCTCAGAAATCAGAGCTAAGGAACTACTAGATAACCAGTGGTTAACAGGCAATAAA  
CTTTCTTCGGTGAGACCAACCAATGTATTAGAGATGATGAAGGAATGGAAAAATAACCCA  
GAAAGTGTGAGGAAAAACAACAGAAGAGAAGAATAAGCCGTCCACTGAAGAAAAGTTG  
AAAAAGTTACCAACCCTGGGGAATGTCCCTGAGACCAATTACACTTCAGATGAAGAGGAG  
GAAAAACAGTCTACTGCTTATGAAAAGCAATTTCCCTGCAACCAGTAAGGCAACTTTGAT  
ATGTGCAGTTCAAGTTTCACATCTAGCAAACTCCTTCCAGCTGAAATCAAGGGAGAAATG  
GAGAAAACCCCTGTGACTCCAAGCCAAGGAACAGCAACCAAGTACCCTGCTAAATCCGGC  
GCCCTGTCCAGAACCAAAAAGAACTCTAAGGTTCCCTCCAGTGTGACAGTACAAAA  
CAAAGCTGCTCTTGTAGCACTTTGATGAGGGGGTAGGAGGGGAAGAAGACAGCCCTATG  
CTGAGCTTGTAGCCTTTTAGCTCCACAGAGCCCCGCCATGTGTTGCACCAGCTTAAAT  
TGAAGCTGCTTATCTCAAAGCAGCATAAGCTGCACATGGCATTAAAGGACAGCCACCAG  
TAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAGATGTACACGAAGGTTTTTTAGG  
GGGGCAGATACCTTCAATTTAAGGCTGTGGGCACACTTGCTCATTTTTACTTCAATTTCT  
TATGTTTAGGCACAGCTATTTATAGGGGAAAAACAAGAGGCCAAATATAGTAATGGAGGTG  
CCAAATAATTATGTGCACCTTTGCACTAGAAGACTTTGTTAGAAAATTAATAAACTTG  
CCATACGTATTACAGCAGAAGTGCTTCAGTCATTTCACATGTGTTCTGTGAGATTTTAGGTT  
GCTATAGATTGTTAAGACAGCTTATTTTAAATGTAGAAAAATAGGAGATTTTGTAACTG  
CTTGCCATTAACTTGCTGCTAAATTTCCCAATGTATTGATTAAATCAATAAAAAACAGATG  
TTACTC

SEQ ID NO: 46\_SGK309\_H  
GGGTCCGCAGCCCCGCCCTCACAGGCCCTCCTCACTCCCCCTAGGTAGATGGCCCCCTCAGG  
GCAGGCCCGGCGGACACCCCTCCCTCTGGCTGGCGGATGCAGTGCCTAGCGGCCGCCCTT  
AAGGACGAAACCAACATGAGTGGGGGAGGGGAGCAGGCCGACATCCTGCCGGCCAACTAC  
GTGGTCAAGGATCGCTGGAAGGTGCTGAAAAAGATCGGGGGCGGGGGCTTTGGTGAGATC  
TACGAGGCCATGGACCTGCTGACCAGGGAGAATGTGGCCCTCAAGGTGGAGTCAGCCCAG  
CAGCCCAAGCAGGTCTCAAGATGGAGGTGGCCGTGCTCAAGAAGTTGCAAGGTTCCGGC  
CTCGGGCAGGGGGATGGGAAGGAAGAGATGATGAAGCCAGGGGCTAAGAGAGGGGAAGGAC

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## FIGURE 2LL

CATGTGTGCAGGTTCAATTGGCTGTGGCAGGAACGAGAAGTTTAACTATGTAGTGATGCAG  
CTCCAGGGCCGGAACCTGGCCGACCTGCGCCGTAGCCAGCCGCGAGGCACCTTCACGCTG  
AGCACCACATTGCGGCTGGGCAAGCAGATCTTGGAGTCCATCGAGGCCATCCACTCTGTG  
GGCTTCTGCA~~CG~~GTGACATCAAGCCTTCAAACCTTGCCATGGGCAGGCTGCCCTCCACC  
TACAGGAAGTGCTATATGCTGGACTTCGGGCTGGCCCGGCAGTACACCAACACCACGGGG  
GATGTGCGGGCCCCCTCGGAATGTGGCCGGGTTTCGAGGAACGGTTTCGCTATGCCTCAGTC  
AATGCCCAACAAGAACCGGGAGATGGGCCGCCACGACGACCTGTGGTCCCTCTTCTACATG  
CTGGTGGAGTTTGCAGTGGGCCAGCTGCCCTGGAGGAAGATCAAGGACAAGGAACAGGTA  
GGGATGATCAAGGAGAAGTATGAGCACCGGATGCTGCTGAAGCACATGCCGTGAGAGTTT  
CACCTCTTCCTGGACCACATTGCCAGCCTCGACTACTTCACCAAGCCCGACTACCAGTTG  
ATCATGTGAGTGTGAGAACAGCATGAAGGAGAGGGGCATTGCCGAGAATGAGGCCTTT  
GACTGGGAGAAGGCAGGCACCGATGCCCTCTGTCCACGAGCACCTCTACCCCGCCCCCA  
GCAGAACACCCGGCAGACGGCAGCCATGTTTGGGGTGGTCAATGTGACGCCAGTGCCTGG  
GGACCTGCTCCGGGAGAACACCGCGGATGTGCTACAGGGAGAGCACCTGAGTGACCAAGGA  
GAATGCACCCCAATTCTGCCCGGGAGGCCCTCTGAGGGGCTGGGCCACAGTCCCCACCT  
TGTCCCCACCCCGGGGGTCTGAGGCTGAAGTCTGGGAGGAGACAGATGTCAACCGGAA  
CAAACCTCCGGATCAACATCGGCAAAGTAACTGCCGCCAGGGCGAAGGGCGTGGGTGGCCT  
TTTCTCTACCCCGATTCCCAGCCTTGTGCCCTGCCCTGTTCTCTCCTAAGCACCTGT  
CCCCCGCAATCTCCTGCTTGCCCGGCCTCTGTTTCCGGTCCCTCCCCGGCACTAGCC  
TCGCTGTGTCTTCCATCATCATCTCTGTCTCCTTCACACTGAGGAGACCATCCGCC

SEQ ID NO: 47\_AA234451\_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCGGCGGCGGCGGCAGGAGGGG  
GAGCAGGTGCTGGCACAAGAGCAGCGGCTTGGGGGAGCCGGCAGCAGCAGTAAACAGCAGC  
AGCAGCCGCGCCGCGCCGCGCCAGTAAACGCGGACCGTACCCAGGGGACTACCCAGCCG  
GCCGGCCCTGGAAGCCGCGCTCGGGTCCCCCGCAGTCCGCGGTGGGGGATGGGCAGGCA  
GTGGCGGTCCCCGCTGCCGAGGGTTAAACCCCGCCGGTCCCGGTCTGAGCTGGACCAGA  
GCCCTCCTCCAGAAACCCCTGCGTCCGCCACGGCCAGGTAAATGGAAACCACCTTGG  
GAACTGGATGCCTGTGTAGCTGTTCTACCATATCAGTGTATTGCAATGAGTGGGGGAGGA  
GAGCAGCTGGATATCCTGAGTGTGGAATCCTAGTGAAAGAAAGATGGAAAGTGTGAGA  
AAGATTGGGGGTGGGGGCTTTGGAGAAATTTACGATGCCTTGGACATGCTCACCAGGGAA  
AATGTTGCACTGAAGGTGGAATCAGCTCAACAACCAAAACAAGTTCTGAAAATGGAAGTT  
GCTGTTTTGAAAAGCTGCAAGGGAAAGACCATGTTTGTAGATTTATTGGCTGTGGGAGG  
AATGATCGATTCAACTATGTGGTCAATGTCAGTTGCAGGGTCCGAATCTGGCAGATCTTCGC  
CGTAGCCAGTCCCGAGGCACATTACCATTAGTACCACTCTCCGGCTGGGTAGACAGATT  
TTGGAGTCTATTGAAAGCATTCACTCTGTGGGATCTTGNCATCGAGACATCAAACCGTCG  
AACTTCGCTATGGGTGCTTTCTAGTACATGTAGGAAATGTTACATGCTTGATTTTGGC  
TTGGCTCGACAATTTACCAATTCCTGTGGTGAAGTCAAGCACATCGGAACAGGGAAATGGGAAGA  
CATGATGACCTTTGGTCCTTATTCTACATGTTGGTGGAGTTTGTGGTTGGTCAGCTGCC  
TGGAGAAAAATAAAGGACAAGGAGCAAGTAGGCTCTATTAAGGAGAGATATGACCACAGG  
CTCATGTTGAAACATCTCCCTCCAGAATTCAGCATCTTTCTAGACCATATCTCTTCTTTG  
GATTATTTTACAAAACCACTACCAGCTTCTTACATCCGTGTTTGACAATAGCATCAAG  
ACTTTTGGAGTAATTGAGAGTGACCCTTTTGAAGTGGGAGAAGACTGGAAATGATGGCTCC  
CTAACAACCACTACTTCTACCAACCCCTCAGTTGCACACTCGCTTGACCCCTGCTGCA  
ATTGGAATTGCCAATGCTACTCCCATCCCTGGAGACTTGCTTCGAGAAAATACAGATGAG  
GTATTTCAGATGAACAGCTTAGCGATGGAGAAAATGGCATCCCTGTTGGTGTGTACCA  
GATAAATTGCCTGGATCTCTGGGACACCCCGTCCCCAGGAGAAGGATGTTTGGGAAGAG  
ATGGATGCCAACAACAAAGATAAAGCTTGAATTTGTAAGGCTGCTACTGAAGAGGAG  
AACAGCCATGGCCAGGCAATGGTCTTCTCAATGCTCCAAGCCTTGGGTACCAATTTCGT

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## FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTCCTACTGGTGCGAAAGTTACGTTCC  
ATTACAGCTTTGAGCTGGAAAAACGTCTGACCCTGGAGCCAAAGCCAGACACTGACAAG  
TTCCTTGAGACCTGGTATAAAATAGTGTATTTTCTTTTAAAGCTTCTAAGGTACCATT  
ATTATTGTTGTCATTGTTGTTATTATTATTGTATATTTCTGTTACATAAAGTCTTCAA  
TAAGAAATCCTTGCATTTTGTAACTGAGTCTATTTCAGCTCCAATTTTCATCCATGTT  
TTTAATTATTATTATCCTGATTCTTAATTATTATAAATTCTATAGCATATCCTTTGGCTT  
TGGAAGCTGAGCAGTAAGAGCTGATGACTTCCTAACACTAGGTACAAGTTAAATGAACAT  
TTTTACAGTAACTTTGTTTAGAAAGTAATCTCTTCCACACAACAGTGTAGTGCTGGAGAG  
GGCATGATAAAGATGGCATTAGGCAGAGATGAGGGGAATACATAAAGGAGGGGAAAAAGT  
AATTACATACACAAGGGACGGTGAGTTCAATTCACCTTTAGTGAAGACCTCTAGGAGTAAG  
ATACTGTGGGAAAAACAGATACCAATAAGTATATCATGCTTGCCCTAGAGAGTTTGCAATC  
TACCTAGAGAGAAAGGAAGGTGAACTTGAGAGATCTATATACATAGGTAAAGATTGTAG  
TGCATGGTTTTGAGGCACATTATCCCTACAACAAATTTTGATAACAGAAGAC

SEQ ID NO: 48\_AA435956\_H  
ACTTTTACTATATTTCTTTGAGATGACTGTTTTTGATTTAGAGGCGAAATCAGCACGTGGT  
GGCTCAAATCTCCTTATGGATAGTGTTCCTTCCTCCAGCTTTTCATGTTCAACTTTTG  
CGGGGCTGGCGTACATCCACCACCAACAGTTCTTCACAGGGACCTGAAACCTCAGAAC  
TTACTCATCAGTCACCTGGGAGAGCTCAAACCTGGCTGATTTTGGTCTTGCCCGGGCCAAG  
TCCATTCCCAGCCAGACATACTCTTCAGAAGTCGTGACCCTCTGGTACCGGCCCCCTGAT  
GCTTGTCTGGGAGCCACTGAATATTCTCTGAGCTGGACATATGGGGTGCAGGCTGCATC  
TTTATTGAAATGTTCCAGGGTCAACCTTTGTTTCTGGGGTTTCCAACATCCTTGAACAG  
CTGGAGAAAATCTGGGAGGTGCTGGGAGTCCCTACAGAGGATACTTGGCCGGGAGTCTCC  
AAGCTACCTAACTACAATCCAGAATGGTTCCTGAAGCTGAAGACCTGGCCTCCAGATGCTAAAA  
GTCTGGAACAGGCTGGGCAGGGTTCCTGAAGCTGAAGACCTGGCCTCCAGATGCTAAAA  
GGCTTTCCCAGAGACCGCGTCTCCGCCCAGGAAGCACTTGTTTATGATTATTTTACGCGC  
CTGCCATCTCAGCTGTACCAGCTTCCTGATGAGGAGTCTTTGTTTACAGTTTTCAGGAGT  
AGGCTAAAGCCAGAAATGTGTGACCTTTTGGCCTCCTACCAGAAAGGTCACCAAGGCTG  
CAGTTTAGCAAATGCTGGTGAAGAAAGGGCGAGATCACCAGGTTCTTCCAGGGCTGT  
ATTTCTGCAGTTTTCGGTTTTTCACTTTCAGCTTACTAAGAAGCTTCAAATCTAATCC  
ATACTGAACAAGGGGCTTTATGTCTCACCTATGACCTGGAATAGTTTAAATATGGTGT  
CAAGGCAATAGTACATAATAGTGAAGAAATTCAGTGAAGGTTATTGTCTATTGTATT  
TGCATAGAATTTAAGTGATTGATTTAAAAAACTGGACATAAATAAGTCTAAGAAG

SEQ ID NO: 49\_AA626859\_H  
AAATGGAGTTGCTGATGGAGTGATCAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA  
TTTCTGTATATACATAACTGTATTACAGAGATATAAAACCTGAAAATATTCTAATAAC  
TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATCTGATTCCAGGAGA  
TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACCTTCTGTGGGAGA  
TACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTGTGTTTTTGCAGAGCTCCT  
GACAGGCCAGCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG  
AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCCA  
TGGCATCAGTATACCTGAGCCAGAAGACATGGAACCTCTTGAGGAAAAGTTCTCAGATGT  
TCATCCTGTGGCTCTGAACCTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT  
AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCAAATTA  
AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGAATCAACTGTTGCCTCT  
CATACCAGGAAGCCACATCTCCCCACACCTGATGGAAGAAAACAAGTCTCCAGTTAAA  
ATTTGATCACCTTCCAACATTTAGGAAAATGTTCTTTCAAGTGCAAAGTAATTTAATAT  
GTACACATTTGTACAAGTGAGATAGGAATTCTCAGTGTTCAAATGCAATGAGCCATA

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## FIGURE 2NN

TGAAAATTAAGATGCCTTCTAGAATTGGTTTGCTCTGATCATTGCTGATTCCCTTTCCCCA  
TGCTTTTACAT

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GAAAATAGCCCTGCGGGAAATCCGTATGCTGAAGTTGAAACACCCAAACCTCGTGAACCT  
CATCGAGGTGTTTTCAGAAGAAAGAGAAAGATGCATCTAGTTTTTGTAGTACTGTGATCACAC  
ACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAGTGT  
GCTATGGCAAACCCCTTCAAGCCCTTAACTTCTGTCAAGCACAATTGTATTCATCGGGA  
TGTAACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG  
ATTTGCACGAATTCTAATTCCAGGAGACGCCTACACAGACTATGTTGCCACCAGGTGGTA  
CCGAGCCCCCGAAGTTCTCGTGGGAGACACGAAGTACGGTTTCTGTAGACGTGTGGGC  
CGTGGGCTGTGTTTTTGCAGAGCTCCTGACGGGTGAGCCACTCTGGCCGGGAAAAATCCGA  
CGTGGACCAGCTTTACCTGATCATCAGGACGTTGGGGAAGCTGATTCCAAGACACCAGTC  
TATCTTTAGGAGTAACCAGTTTTTCCGCGGCATCAGCATACCTGAACCAGAGGACATGGA  
GACTCTTGAAGAAAAATTCTCAAATGTTTCCGCTGTGGCTTTAAGTTTTCATGAAGGGATG  
CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCCAGCTGCTGGAAGTGCCTACTT  
TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCGCAGTGAGGGGAGAAGCCGAAG  
GCGCCAGCAGAATCAACTGCTGCCTCTTATTCCTGGAAGCCACATCTCCCCACACCTGA  
TGGAAGGAAACAAGTCGTCCAGTTAAAGTTCGATCATCTTCCAAACATTTAGGGGACTCA  
TCCTTCCCAGCACATCCTTTTAAATATTGTCTACATAGGAATAAGACGGGAATCCTCAGCA  
TCTCAAATACAGTGAGCGACGTGAACACCGGCACCTCTAATCACCACGGGCTCCTCCC  
CTGTGCTTTTTCCACGCCAGCTCCATCTCCTAAACATTCTCTTTAAATGTTGCAGTATC  
AAAATGGCACATCCGAAAGAGATGCTTCCAGTTTACCAGAGCCGGGCTTCCTCAGGCAA  
TCGGTACTGTGCATCTGTGGAATTATGCTCCGACCTAGGGAAAGATTTCCACGTAGCCGT  
CTCACTTACGCCAGCAGTGGTGTCTGAGCAGACCCAGATCTGCTGGCTGCTGTTTGT  
GGAGGGGATGGCCCTGAGCCCTCTCACTGGAGTTTCTTCTCCGTGCAGCCAGGTCTTACT  
TTAGACTACATTTGTGTTATTGTGGCATGGCAATCGTGAAAGGTGGTCTAGGTTTACCCT  
TGACTCCACAGCAGATGCTAGTCTCCTTCTCGTGAGGAGCTGACAAGTCTGCTTCTAAAA  
CGAAGTAGAGAAAATTCCAAACGTGACCAGTTAGTGGACAGACTACAAGGAATCGACCAC  
CATACCACAGTAACGCCCTGGATCCCTGGCTGCCCACTCTAAGGCTATCCTGGTT  
CACCATGGTTTCTCTTTCTTTTCTTTTCTTTTAAATCTATTTGTACATATGAGAAAGAGGC  
AGAGGGGCGAGAGAAACCTCGTGTGTGAAAATCAAAAGACAAGCAGGAGGCCAGCCTAAG  
CTACATAGCAAGGCCTTTTCTCTACACCCATTCTCTAAGGTTGCTTAAACCCAAGTCCCT  
GCTGCTGATTGTATAAACTATGAATAAGTTCTACATATGTAGGACATATTGTTGTCAATTG  
TTGAAATATCTAAGGATCTTGGTAGAAGCAGAAGTGTCTAAATATTCTCCACACTGGTG  
AGTATCTTGGCATTTCATTTCTGACCTCATCAGATGAACACATCAAAGGATGAGTATG  
TATCACTTTGCATCTTAGAATTCTACCTGTTTGTAGCTGCGTTAAACCTTGTGAAAGGGCG  
GGGCCATAACTGAACCTGTGGAGTTCTTGCTGTGTGAGGAAACCTCTGGTTTGTCT  
CCAGCATGGAAGAAAACAGCTATAGTCAACCTACCTGAAAGTAGAAATTCAAAGTCACT  
GTCCTTGACTACATATGCAGTCCAAGGCCACGCTGGGCTACACTTCTCCAGGCATGAAGG  
TCCGTGTTTGTATCAAGGGGCGAGGAAAGGAGAGTCCAAGGTCAAGGCCAGCCAGGCTGC  
ATAGTGAGTTGAGGCTCTTCAAGGAAAGGAAAGGAACTAATAGGAGTCGTTGAAGGTAG  
CCACCGGCCATTTCTCTAAATATCATTCTGCTGAAAAGGGGGCTTAGTTTAGTTAGAA  
GCATTAATGTATGTAGAAGCTGGGCTATTTCAAGATTATTTGAAATTGTAGCTATTGTAA  
TTAGCACTTAATACTAAGCTAGCATTATGGTAGTCTAACTATTAGAGTTTACTACAAAG  
AGGTTTTGATTGAATTATTAACATATAATATGGATTTTAAAAATTTAAGATGTTTAA  
GAAAGCTATATAAGATTAAACATTTTTGTGGCTGTATTTTGTGTATATACCTTGGTTG  
TTCTTTAAATTATTTTAAATAAAGCCAGAAACATT

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## FIGURE 200

SEQ ID NO: 51\_AA397553\_H  
ATGCCCAATTTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAAC  
TTGCAGCCGTTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCG  
AAGCACAAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGACCCCCGAAGCA  
GCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCC  
GACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGAACGTCGT  
GGATCAGATCGGAGCGACCGCCTGCACAAACATCGTCAACCACGACAGGCGTTCCCCG  
GACTTACTAAAAGCTAAACAGACCGAAAAAGAAAAAGCCAAAGTCTCCAGCAAGTCG  
GGATCGATGAAGGACCGGATATCGGGAAGTTCAAAGCGTTTGAATGAGGAGACTGATGAC  
TATGGGAAGGCGCAGGTAGCCAAAAGCAGCAGCAAGGAATCCAGGTCATCCAAGCTCCAC  
AAGGAGAAGACAGGAAAGAACGGGAGCTGAAGTCTGGGCACAAAGACCGGAGTAAAAGT  
CATCGAAAAAGGGAAACACCCAAAAGTTACAAAACAGTGGACAGCCCAAAACGGAGATCC  
AGGAGCCCCCAGAGGAGTGGTCTGACAGCTCCAAACAAGATGATAGCCCCCTCGGGAGCT  
TCTTATGGCCAAAGATTATGACCTTAGTCCCTCACGATCTCATACCTCGAGCAATTATGAC  
TCCTACAAGAAAAAGTCTTGAAGTACCTCGAGAAGGCAGTCGGTCAGTCCCCCTTACAAG  
GAGCCTTCGGCCTACCAGTCCAGCACCCGGTCACCGAGCCCCCTACAGTAGGCGACAGAGA  
TCTGTGAGTCCCTATAGCAGGAGACGGTCGTCCAGCTACGAAAGAAGTGGCTCTTACAGC  
GGGCGATCGCCAGTCCCTATGGTGAAGGCGGTCCAGCAGCCCTTTCCTGAGCAAGCGG  
TCTCTGAGTCCGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCCT  
GCATATTCAAGACATTCTCTCTCATAGTAAAAAGAGATCCAGTTCACCGAGTCGT  
CATTCAGTATCTCACCTGTCAGGCTTCCACTTAATTCCAGTCTGGGAGCTGAACTCAGT  
AGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGTCAGCAAGATGGATGGAAAGGAGTCC  
AAGGGTTACCTGTATTTTTGCCTAGAAAAGAGAACAGTTCAGTAGAGGCTAAGGATTCA  
GGTTTGGAGTCTAAAAGTTACCCAGAAGTGTAAAATTTGGAATAATCTGCCCCAGATACT  
GAACTGGTGAATGTAAACATCTAAACACAGAGGTAAAAAATTTCTTCAGATACAGGGAAA  
AGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCCAAAGGAGACAGAAACA  
TCAGAAAAGGAGACCCCTCCACCTCTTCCACAAATTGCTTCTCCCCACCCCTCTACCA  
ACTACTACCCCTCCACCTCAGACACCCCTTTGCCACCTTTGCCCTCCAATACAGCTCTT  
CCACAGCAACCACCTCTGCCTCCTTCTCAGCCAGCATTAGTCAGGTTCTGCTTCCAGT  
ACTTCAACTTTGCCCCCTTCTACTCACTCAAAGACATCTGCTGTGTCTCTCAGGCAAT  
TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAAACAGCTGCTATTCCA  
CACCTGAAAACCTTCAACGTTGCCTCCTTTGCCCCCTCCACCCCTTATTACCTGGAGGTGAT  
GACATGGATAGTCCAAAGAAACTCTTCTTCAAACCTGTGAAGAAAGAGAAGGAACAG  
AGGACACGTCACTTACTCACAGACCTTCTCTCCCTCCAGAGCTCCCTGGTGGAGATCTG  
TCTCCCCCAGACTCTCCAGAACCAGGAATCACACCACCTCAGCAACCATATAAAAAG  
AGACCAAAAATTTGTTGCTCGTTATGGAGAAAGAACAAACAGAAAGCGACTGGGGG  
AAACGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCAA  
GTATATAAAGCCAGGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGTGAGACTA  
GACAATGAGAAAGAGGGCTTCCCAATCACAGCCATTCTGTGAATCAAAATCCTTCGTGAG  
TTAATCCACCGAAGTGTGTTAATGAGGAAATTTGTGAGTATATGGACCATGACTTA  
GATTTCAAGAAGGACAAAGGTGCCTTTTACCTTGTATTTGAGTATATGGACCATGACTTA  
ATGGGACTGCTAGAATCTGGTTTGGTGCCTTTTCTGAGGACCATATCAAGTCGTTTCTG  
AAACAGCTAATGGAAGGATTGGAATACTGTCAAAAAAGAAATTTCTGCTATCGGGATATT  
AAGTGTCTAATTTTGTGTAATAACAGTGGGCAAATCAAACCTAGCAGATTTTGGACTT  
GCTCGGCTCTATACTCTGAAGAGAGTGCCTTTTACCTTGTATTTGAGTATATGGACCATGACTTA  
TACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACCAGCCATAGATGTTTGG  
AGCTGTGGATGATTCTTGGGGAACCTATTCAAAAGAAGCCTATTTTCAAGCCAATCTG  
GAACTGGCTCAGCTAGAATGATCAGCCGACTTTGTGGTAGCCCTTGTCCAGCTGTGTGG  
CCTGATGTTATCAAACCTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGG

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FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTCATTCTTCTGCAGCACTTGATTATTGGACCACATG  
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT  
AAAGATGTGCGAACTCAGCAAAATGGCTCCTCCAGACCTCCCCACTGGCAGGATTGCCAT  
GAGTTGTGGAGTAAGAAACGGCGACGTCAGCGACAAAGTGGTGTGTAGTCGAAGAGCCA  
CCTCCATCCAAAACCTTCTCGAAAAGAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG  
AACAGCAGCCCGAGCACCACCTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT  
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTATTA  
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC  
CACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTG  
ACGGAAGCTACTTCCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAG  
GAAGCACCCCTCTGCCCCAGTGATCCTGCCTTCAGCAGAACAGATGACCCCTGAAGCTTCA  
AGCACACCAGCTGCATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC  
CAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG  
CCCCGAAGAACTCCACAATGCCACAGGAGGAGGCAGCAGCATGTCTCTCACATTCTT  
CCACCAGAGAAGAGGCCCCCTGAGCCCCCGGACCTCCACCGCCGACCTCCACCCCTT  
CTGGTTGAAGGCGATCTTTCCAGCGCCCCCAGGAGTTGAACCCAGCCGTGACAGCCGCC  
TTGCTGCAACTTTTATCCAGCCTGAAGCAGAGCCTCCTGGCCACCTGCCACATGAGCAC  
CAGGCCTTGAGACCAATGGAGTACTCCACCCGACCCCGTCCAAACAGGACTTATGGAAAC  
ACTGATGGGCCTGAAACAGGGTTTCACTGCCATTGACACTGATGAACGAACTCTGGTCCA  
GCCTTGACAGAATCCTTGGTCCAGACCCTGGTGAAGAACAGGACCTTCTCAGGCTCTCTG  
AGCCACCTTGGGGAGTCCAGCAGTTACCAGGGCACAGGGTCAGTGCAGTTTCCAGGGGAC  
CAGGACCTCCGTTTTGCCAGGGTCCCCTTAGCGTTACACCCGGTGGTCCGGCAACCATT  
CTGAAGGCTGAGGGAAGCAGCAATTCTGTGGTACATGCAGAGACCAATTGCAAACTAT  
GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG  
GGCCCAACTCAGTCTTCTGCTTATGGAAAACCTATCGGGGGCCTACAAGAGTCCCACCA  
AGAGGGGGAAGAGGGAGAGGAGTTCTTACTAA

SEQ ID NO: 52\_AA789239\_H

TGAAAATGGAGATGTATGAAACCCTTGGAAGAGTGGGAGAGGGAAGTTACGGAACAGTCA  
TGAAATGTAAACATAAGAATACTGGGCAGATAGTGGCCATTAAAGATATTTTATGAGAGAC  
CAGAACAACTGTCAACAAAATTGCGATGAGAGAAATAAAGTTTCTAAAGCAATTTTCATC  
ACGAAAACCTGGTCAATCTGATTGAAGTTTTTAGACAGAAAAAGAAAATTCATTTGGTAT  
TTGAATTTATTGACCACACAGTATTAGATGAGTTACAACATTATTGTCTATGGACTAGAGA  
GTAAGCGACTTAGAAAATACCTCTTCCAGATCCTTCGAGCAATTGACTATCTTCACAGTA  
ATAATGTAATCATTCAGAGATATAAAACCTGAGAATATTTTAGTATCCCAGTCAGGAA  
TTACTAAGCTCTGTGATTTTGGTTTTGCACGAACACTAGCAGCTCCTGGGGACATTTATA  
CGGACTATGTGGCCACACGCTGGTATAGAGCTCCCGAATTAGTATTAAAAGATACTTCTT  
ATGGAAAGTATGTGCCTGTGGATATCTGGGCTTTGGGCTGTATGATCATTGAGATGGCCA  
CTGGAAATCCCTATCTTCTAGTAGTTCTGATTTGGATTACTCCATAAAATTGTTTTGA  
AAGTGNGATTATGCCAGAACTGAAAGCTAAATTAAGTGCAGGAAGCAAAAGTCAATTCAT  
TAATAAAGCCAAAAGAGAGTTCTAAAGAAAATGAACTCAGGAAAGATGAAAGAAAAACAG  
TTTATACCAATACACTGCTAAGTAGTTCACTTTTGGGAAAGGAAATAGAAAAAGAGAAAA  
AGCCCAAGGAGATCAAAGTCAGAGTTATTAAAGTCAAAGGAGGAAGAGGAGATATCTCAG  
AACCAAAAAAGAAAGAGTATGAAGGTGGACTTGGTCAACAGGATGCAAATGAAAATGTTT  
ATCCTATGTCTCCAGATACAAAACCTTGTAACCATTTGAACCAACCAACCCCTATCAATCCCC  
GCACTAAGTGTAAATGGCTTGAAAGAAAATCCACATTGCGGAGGTTCTGTGACAATGCCAC  
CCATCAATCTAATAACAGTAATTTGATGGCTGCAAATCTCAGTTCAAATCTCTTTACC  
CCAGTGTGAGGTTAACTGAAAGAGCAAAAAAGAGACGCACTTCTTACAATCTATTGGAC  
AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGGTCTTATCAAAGCCAAATGGAGAAGG  
GTATATTTAATGAGCGAACAGGTCACAGTGACCAATGGCAAATGAGAACAAAAGGAAGC

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PCT/US00/14842

WO 00/73469

## FIGURE 2QQ

TGAATTTTCCAGATCTGACAGGAAAGAATTCCATTTTCCAGAATTGCCTGTCACAATAC  
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAAATGCTGAAGAGGGAGTCAA  
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC  
AAGAGTTTATTCCCTTATCTCTGCTGTCTGCCTGCTGCTCTATTTTACAAAATATTGCT  
CTCAGCTAACTATCAGGGTGGAGATGGCCATTGCGAGGGGAAGAATTGAAGAGAAACAG  
GTTTTTTTTCTGGTAGTGTCTTTCTTTTACATAGTCCAAAAAATACAAGATGACAACCTC  
TTCCCGTTTATTTATCTACAATAGAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC  
ATGTGCATGAGCATCATCCAGCTTTTTTTGTTAGCAAAACATTTACTGTTTTCTTTTCCC  
TTTTAAGACTCTGTTGATGTGATAATTTGATTGGAATTATAAAGTCATCTCTCTCTGC  
CTTGAA

SEQ ID NO: 53\_AA124976\_M  
CTGGCAGATATAGTTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT  
GATCTTTTTCGTCACGATTACTTTACTAGAGATGGATTTATTGAGAAATTCATACCAGAG  
CTGAGAGCTAAATTATTACAGGAAGCAAAGGTTAATTCATTTATAAAGCCAAAAGAGAAT  
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTACCAACACCCTGCTC  
TATGGAAATCCATCACTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC  
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCCAGACCAGAAGAAGCCA  
GAGTATGAAGGCGACCACCGCCAGCAGGGCACAGCTGATGACACACAGCCCTCATCACTG  
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCTCTCAATCCCAGTGAGAATTCTGAC  
GGTGTCAAAGAAGACCCACACGCTGGGGGTGTATGATAATGCCACCTATCAACCTGACA  
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTCAAACCTTTCCCACCCCAATTCACGGTTA  
ACTGAAAGAACA AAAAGAGACGCACTTCTTCACAACTATTGGACAGACTTTGTCTAAT  
AGCAGACAAGAGGACACAGGTCCCAACAAGTCCAAACAGAGAAAGGTGCATTTAATGAG  
CGAACAGGTGAGATGACCAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAA  
TGCGCAGGAAAGAATTCCATTTCCCTGAACTGCCATTACAGTGCAGGCGAAGGAGATG  
AAAGGGATGGAAGTTAAACAGATAAAAGTGTGAGAGAGAATCAAAGAAAACAGATTCA  
TCTAAAATACCAACTTTACTTAGTATGGACCCAAATCAAGAAAAACAAGAGGGTGGAGAT  
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTTCCCGATAGTGCTTT  
GTCTTTTAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTATTTTATATAC  
ACTAGAATGTACATAGGTTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT  
CTATTTTTTTGGTTTTGCTAGCAAAATTTTACAATTTTTCTCTATCTTCCAAAACTGT  
TATTTTGATGCTGTGATTTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCTCTCCTGCTG  
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG  
AGACTCAAACCTCATAAGCCAGGGGTCTCCTGGGAAGCACTGGCCTCTCAAGTGGATGC  
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCACATGATGAAAGA  
CATTCTATTGTCCCCAGTGAAGCATTATAGTACTTACATAACATGTTACAGTGATATGA  
TGTTCCCTAGGTTAAACTCCTTGAGATGAACTATTTCTGCACTTCTGACTCCCCCTAGT  
CTAATAGTTCCCTTCATTTAGCCAGAAGAATTTCTGGAAGAAGCGATGCACAACCTGGGA  
AAGGTTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA  
GTTAACAT

SEQ ID NO: 54\_AA575635\_M CCRK\_M  
AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCCGGTCTTCTCTCCGGAT  
GGTGGTGCCTCTACACACATCAGGTGGCCACCAGGTGGTACCGAGCTCCTGAACTCCTG  
TATGGCGCTCGGCAGTATGACCAGGGCGTTGACCTATGGGCTGTGGGCTGCATCATGGGA  
GAGCTGTTGAATGGGTCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACCTGTGCTGT  
GTGCTTCGCATCCTGGGTACCCGAGTCCTCGAGTCTGGCCGGAGATCACAGAGCTGCCT  
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAAGTGGCCCTGGAGGAGGTGCTGCCT  
GATGCCTCTCCCCAGGCCTTGGACCTGCTGGGCCAGTTCCTCCTCTACCCTCCACGACAG

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## FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTCACAGCGCCTCTGCCTGCC  
CATCCATCCGAGCTGCCAATTCCTCAGCGCCCAGGGGGACCTGCACCCAAGGCTCACCCA  
GGGCCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC  
CCAGAACTGATTTCGGCCCTTCATCCCAGAGGGGTGAGATGTTGGTCCAGGCCTTCCTGCT  
CGCCCTAGGAGCACCTCTTCTGATTTGCCTCCATGGCCTCCCCACGGCTATATATACCA  
CACCTGGTCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCGTGAGA  
TGTTTCATCCCAGCAGAGAAAGAGACTCACGTCTACAGACAAAGCCTCCAGAACTGCTA  
GCTGTGTCCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC  
AGGCTCTGTCCCCCTCTTCAAGGACATTGGTACTACAGCACCACCTGGTGGAAGCACAGAG  
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT  
CCACTGGGTGAGATTTGAGGTTTCATATAAAAGCCCTGGGTGTTTTCTGTCTAATTGCACC  
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGGCCTTGATTCACAGGGGTGAGGACT  
CAGAAGGGGCCCTCCTGTGAAGGCCATTTGGGTCTCAGGCTTCCCATGCTATTCACGGGA  
CTTGAGTGCTCATTTGGGAGCGAGGGTCCAGAAGCTGAGGCCCAGGGATGGACAGTCCAG  
TTCCCGAAGCCCACTTCCCACATGTCGGGTGGGTGAGTCACTGAGCCTGAGGCTGCCTTG  
CAGATGCGGAAGCAGGCATTCCTGGAATCCACTCAGTAAATAAATTCAGTGTGACTCAG

SEQ ID NO: 55\_AA631990\_H

GAACAACAATAACAGAATAAGGAAGAAAATCTCATGATTACCTCAATAAGTACAGAGAAA  
TCTGGTCACTCACTATCCATTCATGATTACAACCTCTTCAATACTATCGCGGCCGAGGA  
GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTGCGGAGATG  
CGGCATTCCAAAAGAACTCACTGTCCTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA  
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG  
CATTGTAAACCACATCACCAGTTTAAAGAATCTGATTGTCAATTATTTAGAAGCAAGGTCC  
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT  
GAAGGATATGTTCCCTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGC  
AGTAAATCTTCAGTCCCGCAGCAGGAGAAGCAGTCCATAAAGGAAGCGCAATAGCACTGT  
TCAAGTCATCAGTCACGTTTCGNATGAAATCGTGACACTTTGGGTGAAGGACCTTTGGC  
AAAGTTGTAGAGTGCAATTGATCATGGCATGGATGGCATGCATGTAGCAGTGAATAATCGTA  
AAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTTCAGAAATCCAAGTATTAGAGCACTTA  
AATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCAT  
CATGGTCATGTTTGTATTGTGTTTGAACACTACTGGGACTTAGTACTTACGATTTTCAATAA  
GAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC  
CAGTCAATAAATTTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT  
ATTTTGTGTTGTGAAGTCTGACTATGTAGTCAAATATAATTTCTAAATGAAACGTGATGAA  
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT  
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCAATTTGGCT  
TTAGGTTGGTCTCAGCCTTGTGATGTTGGAGCATAGGTTGCATTCTTATTGAATATTAC  
CTTGGTTTTCAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA  
ATATTAGGACCCATACCACAACACATGATTAGAAAACAAGAAAACGCAAGTATTTTAC  
CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC  
AAACCGTTGAAGGAATTTATGCTTTGTGATGAAGAATGAGAACTGTTTGACCTG  
GTTGGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCGAG  
CATCCTTTCTTTGACTTATTAATAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA  
CTTCTCTAGAAGAGATTACTTAAGACTGTGTCACTCAACTAAACATTCTAATATTTTTGT  
AAACATTAAATTATTTTGTACAGTTAAGTGTAATATTGTATGTTTTGTATCAATAGCAT  
AATTAAGTGTAAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAATAATTTT  
TCTTTTGAATTAACATTTTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT  
GTGATTGATCTTGCTTTTGTACATGGAGGTCACTCTGAAGTGATTTTTTTTGTAGTAAA  
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGA

FIGURE 2SS

ACTTAACTTTAAAAGTTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAAGTCTAG  
ATAAGCAGGTACTAGAAACCAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATT  
TTAAGTGTGTATTCTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAA  
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAAACCATACACACTTTATTT  
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGT  
GAGTCACAGATATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTAAATACCAAGTCC  
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAAATACGTAAACCTAT  
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG  
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAAATTAATTGA  
TTGGTTACATAAACTTTTGAAGTTCAAT

SEQ ID NO: 56\_AA557536\_H

AGTAAGGCCCGCGGGCGTCTGGCCGCCATGTGCACCGTAGTGGACCCTCGCATTGTCC  
GGAGATACCTACTCAGGCGGCAGCTCGGGCAGGGGAGAACATTCCGGGAAATCACGCTCC  
TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCTTGCCCAGGTACAGATCTCTCCA  
GACAGGAGAGAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCCTCGGCCTTCCAGCC  
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACC  
TGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTGTTGAGTTTATGGACACTGACC  
TGAACGCAGTCATCCGGAAGGGCGGCCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT  
ACCAGTCCCTGCGGGCCACCCGGTTCTCCTCACTCGGGGCACGTTGTGCACCGGGACCAGA  
AGCCGTCCAATGTGCTCCTGGATGCCAACTGCACAGTGAAGCTGTGTGACTTTGGCCTGG  
CCCGCTCCCTGGGCGACCTCCCTGAGGGGCCTGAGGACCAGGCCGTGACAGAGTACGTGG  
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTCTCGCACCGCTACACCGCTTCTCT  
GCCCCAGATACACCCTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC  
TGCGGGGGAGACCCCTGTTCCCGGCACGTCCACCCTCCACCAGCTGGAGCTGATCCTGG  
AGACCATCCCACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC  
CGCCAGACACCTCCCCAGAGGCCTTGACCTCCTTAGGCGACTCCTGGTGTTCGCCCCGG  
ACAAGCGTTAAGCGCGACCCAGGCACTGCAGCACCCCTACGTGCAGAGGTTCCACTGCC  
CCAGCGACGAGTGGGCACGAGAGGCAGATGTGCGGCCCGGGCACACGAAGGGGTCCAGC  
TCTCTGTGCTGAGTACCGCAGCCCGTCTATCAGATGATCCTGGAGTGTGGAGGCAGCA  
GCGGCACCTCGAGAGAGAAGGGCCCCGAGGGTGTCTCCCAAGCCAGGCACACCTGCACA  
AACCCAGAGCCGACCTCAGCTGCCTTCTAGGACACCTGTGCAGGGTCCCAGACCCAGGC  
CCCAGAGCAGCCAGGCCATGACCCTGCCAGCACGAGTCCCCCGTGCAGCCAAGAACG  
TTCCAGGCAGAACTCCGCTCCCCTGCTCCAACTGCTCTCCTAGGGAATGGGGAAAGGC  
CCCCTGGGGCGAAGGAAGCGCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGGAGGG  
GAGCTGCGCCCTCCCTGACCTCCAGGCTGCGGCTCAGGTGGCCAACCAGGCCCTGATCC  
GGGTGACTGGAACCGGGGCGGTGGGGTGAAGGTGGCCAGCGTACAACAGGTCCCTCCCC  
GGCTTCCCTCCGAGGCCCCGGCCCCGGGAGGATGTTTCAACACCTCTGCCTTGAGGGTG  
CCCAGGGGGGTGCCAGGGCTTTGCTTGGAGGCTACTCCCAAGCCTACGGGACTGTCTGCC  
ACTCGGCACTGGGCCACCTGCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC  
CTTCACTGGCCCTCTGTTCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG  
CACCCCTTAGCCCTCCCTGCTTTGCTTGGCCCGTTGAAGTTCCAGGGAGCTTGCCCGGGT  
CTCCTCGGGGGAGCAGATGAGGGCCCTGCC

SEQ ID NO: 57\_N28606\_H, MOK\_H

ATGAAGAACTATAAAGCAATTGGCAAAATAGGAGAGGGAACGTTTTCTGAAGTTATGAAG  
ATGCAAAGCCTGAGAGATGGAACTACTATGCATGTAAACAAATGAAGCAGCGCTTTGAA  
AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC  
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGACAGAAAATCTGGTTCTCTTGACTA  
ATATGTGAACCTTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATACCCATTA

## FIGURE 2TT

TCAGAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTAC  
 AGAAATGGAATATTTACAGAGATGTAAACCAGAAAAATACTAATAAAGCAGGATGTC  
 CTGAAATTAGGGGACTTTGGCTCCTGCCGGAGTGTCTATTCCAAGCAGCCGTACACGGAA  
 TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTTCTACACG  
 TACAAGATGGACCTGTGGAGCGCCGGCTGTGTCTTCTACGAGATCGCCAGTCTGCAGCCC  
 CTCTTTTCTGGAGTAAATGAACTGGACCAATCTCAAAAATCCACGATGTCTATCGGCACA  
 CCCGCTCAGAAGATCCTCACCAGTTCAAACAGTTCGAGAGCTATGAATTTTGATTTTCTT  
 TTTAAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC  
 CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCACCAGGCCCTG  
 CAGCAACCTACTTCCAAGAACAGAGGAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA  
 AAAGCTGGCTTTCCGGAGCACCTGTGGCACCGGAACCACTCAGTAACAGCTGCCAGATT  
 TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCTCCCAAGAGA  
 CGAGGACCGGCCTATGTCTGGAAGTGCCTAAAGCTTTCCGGAGTGGTCAGACTG  
 TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG  
 CCGGTGCTGAGACCCTTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCGCAGAAGGAC  
 CTTAAGCCTGCCCCGCAGCAGTGTGCGCTGCCACCATAGTGCGGAAAGGCGGAAGATAA

SEQ ID NO: 58\_AB023153\_H, ICK\_H  
 ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCTCTGCTG  
 GGAAGAAGCATTGAGTCTGGGAGCTGATCGCTATTAAAAAATGAAAAGAAAATTTTAT  
 TCCTGGGAGGAATGCATGAACCAACGGGAGGTTAAGTCTTTAAAGAAGCTCAACCATGCC  
 AATGTAGTCAAATTAAAAGAAGTTATCAGGGAATATGATCATCTTTATTTATCTTCGAG  
 TACATGAAGGAAAATCTTTACCAGCTCATTAAAGAGAGAAAATAAGTTGTTTCTGAGTCT  
 GCTATAAGGAATATCATGTATCAGATATTACAAGGACTCGCATTTATTCACAACTCGGC  
 TTCTTTTATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGGACCAGAACTTGTGAAA  
 ATTGCAGACTTTGGTTTGGCCCGAGAAAATACGATCAAAACCTCCATATACAGATTATGTA  
 TCTACCAGATGGTACAGGGCTCCAGAAGTACTCCTGAGGTCTACCAACTACAGCTCCCCC  
 ATTGACGTCTGGGCGGTGGGCTGCATCATGGCAGAAGTTTACACCCTCAGGCCACTCTTC  
 CCTGGAGCCAGTGAAATTGACACAATATTCAAAATTTGCCAAGTGCTGGGGACACCAAAA  
 AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCAATGAACCTCCGTGGCCACAG  
 TGTGTACCCAATAACTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC  
 CTGAGAGACATGCTTCAGTGGGATCCCAAGAAACGACCAACAGCTAGTCAGGCACTTCGA  
 TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCACACAAAACCTTCAGGATTCA  
 GAAAAACCACAGAAAGGCATCCTGGAAAGGGCAGGCCACCTCCTTATATTAAGCCAGTC  
 CCACCTGCCCAGCCACCAGCCAAGCCACACACACGAATTTCTTCACGACAGCATCAAGCC  
 AGCCAGCCCCCTCTGCATCTCACGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC  
 CCAAGCCATCTCCAGGAGGACAAGCCAAGCCCCGTGCTTTTCCCATCCCTCCACAACAAG  
 CATCCACAGTCGAAAATCACAGCTGGCCTGGAGCACAAAAATGGTGAGATAAAGCCAAAG  
 AGTAGGAGAAGGTGGGGTCTTATTTCCAGGTCAACAAAGGATTGAGATGATTGGGCTGAC  
 TTGGATGACTTGATTTTCACTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA  
 CAGAGTGATGACACTCTCTGCAGGTTTGAGAGTGTGTTTGGACCTGAAGCCCTCTGAGCCT  
 GTGGGCACAGGAAACAGTGCCCCCAGACGTCATATCAGCGGCGAGACACGCCACCT  
 CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTTGCTGGGATCAGT  
 ATAAGAAAATGGCATACTCTCGAATCCAGGCAAGGAATTTATTCACCTAATCCATGGTCT  
 AGTTCTGGCTTGTCTGGAATCTTTCAGGGACAATGTGAGTAATCAGCAAAGTAAATTC  
 GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAACTATGTCCCTTCTTTCTG  
 AAAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTTAGCACCTATTCCAGACCCTCC  
 CCTGGTTATTCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATCTTGGACACC  
 CAGCCTAGAAGCACTCCTGGGTTGATACACGGCCTCCAGCCGCCAGCCAGTGCATGGC  
 CGGACAGACTGGGCTTCCAAGTACCCATCCCGCGGTGA

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PCT/US00/14842

FIGURE 2UU

SEQ ID NO: 59\_AA839940\_M  
AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG  
AGAGGACCAAGCTTGGCTACAAGGGACTGGAGAGATGAGACTGTTGGGACCACAGACCTG  
CAGCAAGGCATAGACCCAGGAGCAGTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT  
GGCCAGGAAGAAGCTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT  
CTAGATGACAGCGCAGCACCCCCAGCCCCCTTTGAACACCGGGTAGTGAGCATCAAAGAT  
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTTCGGTTT  
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC  
AAAGTGAAGAACGTAAAGGACCGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG  
CTCAGCCACGTAAACTTGATCCAACCTTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT  
CTGATCATGGAGTATGTGGATGGAGGCGAACTCTTGACCGGATCACGGATGAGAAGTAC  
CACCTCACTGAGTTGGATGTGGTCTTGTTCACGAGGCAGATCTGTGAGGGTGTGCATTAC  
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACATATTGTGTGTGCAGC  
CAGACAGGGCATCAAATTAAGATCATTGACTTTGGGCTGGCTAGAAGATACAAGCCTCGG  
GAGAAGCTAAAGGTGAACCTTGGTACTCCGGAGTTCCTGGCCCCAGAAGTTGTTAACTAT  
GAGTTTGTGTCATTTCCAACAGACATGTGGAGTGTGGGAGTTATCACTACATGCTACTC  
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC  
TGCAGCTGGGATTTTCGATGCTGATACCTTCAAAGGGCTGTGCGAGGAAGCCAAGACTTT  
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTCCCTGAAA  
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAACGTTTCGCTCAGATCC  
CAACAACCTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG  
GCTGCAGTCAACAGGCTACGGAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC  
CACTGGGCCTGGGAATTTCTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA  
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTCTTATTTTGCAAAGAATGATGGA  
AGGAAGCAAGAAAGAAAGAAAGAAAGAAAGGGGGAAGAAAGGAAAGGCAAGCAAGCAA  
GGAAACAGGCTACGTTGTTGCTCTTCTTGTAGGTGAAAGTGTGTTTTATTAAAGCCCTAG  
GAATGTTTTTCTGCCTCGTAAGGTGAGGCTCTCATATGCTGCTTACCCCGCACCC  
TTCCTTTTGGTAATAAGAGCAGGCACGCTCAGGATGGGCAGGGAAATCTTCTGGCTTT  
TGGTCAAATTTGAATTTCTAACTTGTGATGATTAAAGAAGCCAGTAGGGAGGGATG  
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA  
TTCTTAAAGAATTAATAAAATATATTTTTAAAGGAG

SEQ ID NO: 60\_AA460132\_H  
GGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAACCACTTACAGGCCGGAAG  
TGTCCGGGGTGGACGATTTCGGGTAGCCGAAGAAGTCCCAGGATTGCCGAAGAAGTCCCA  
GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAGAGACAGCTGATCGGTGGAG  
CTGTTGCGCGGAGCAGTCATGGCGGCGCCAGAGCTACTACGCGGCGGATGGCGAGGAG  
CCGCCCCGGAGGCTGAGGCTCTGGCCGCGAGCCCGGAGCGGAGCAGCCGCTTCTTGAGC  
GGCCTGGAGCTGGTGAAGCAGGGTGGCGAGGCGCGCGTGTTCGCTGGCGGCTTCCAGGGC  
CGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACCGGCACCCGGCGCTGGAGGCG  
CGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCCGGCGCTCCTCCGCTGTGCGCGCGCT  
GGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTTCCAACCTGCTTATATATGGAA  
GAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTCAGTCCACTATGGAGACTGAAAAA  
ACTCCCCAGGGTCTCTCCAACCTAGCCAAGACAATTGGGCAGGTTTTGGCTCGAATGCAC  
GATGAAGACCTCATTGATGCTGATCTCACCACCTCCAACATGCTCCTGAAACCCCCCTG  
GAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTCAATTCAGCACTTCCAGAG  
GATAAGGGAGTAGACCTCTATGCTCTGGAGAAGGCTTCCCTCAGTACCCATCCCAACACT  
GAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCCTCCAAAAGGCCAGGCCA  
GTGCTAAAAAATTAGATGAAGTGGCCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG  
AAGAATGTGTATGACAACCACACAGTGAAGCTCTTTTTTCAAAGTAAATTTGAAGAA

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## FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTAAAGTGGTATGTG  
ATCGTGTCAATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCATGTTCT  
AGGCAGAAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCAGATTGTGACATGTA  
TATCTCAGATACATGGGTGTGGCATTGAACCACATAATGAGAACATTATTCTCTTTTAG  
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT  
AACCCAGTGTTTTTTTTGTGTTGTTGTTGTGTACATGTTATATTTATTTTGAACCAGTTT  
AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

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CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG  
GACACGGAGGAGGGGTAGAGGTGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCC  
TTCCGGCGGCACGAGGAGAAGATCCAGACCGTGTTCGAGCAGCTGGTGCTGGTGACCAC  
CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTC  
ATCTTCATCACAGAGTACGTGTCTCATCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAG  
AAGAACCACAAGGCCATGAACGCCCCGGCCCTGGAAGCGCTGGTGCACGCAGATCCTGTCT  
GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGAC  
ACCATCTTCATTAGCACAACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC  
TCCAATGCACTTCCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACCTCGG  
AACCTGCACCTTCTCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC  
TTCTCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATCCAGACCAATGGGGAC  
ACCCGGGTACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG  
CGGGAGTTCATCCTTTGCTGCCTGGCCCCGGGACCCCTGCCCGCCGGCCCTCTGCCACAGC  
CTCCTCTTCCACCGCGTGTCTTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC  
TTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG  
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCCGCAGGCCCCCGCTGCAGTGGCGG  
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGATGTGAGGAATGGAATC  
TACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTGCCCGCTGTGCTGGCCCCA  
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAGCCCTTTGACTCTGAGACC  
AGAAAGGTTCATCCAGATGCAGTGCAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCAT  
CTCACTCTGCTTCTGGTGTGGAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTC  
CCAACGGACAGCGCCAGGACCTCGCCTCGGAGCTCGTGCATATGGCTTCCTCCACGAG  
GACGACCGGATGAAGCTGGCCGCTTCTTGGAGAGCACCTTCCTCAAGTACCGTGGGACC  
CAGGCCTGACCCGGAGCCCCAGCCCCAGGACCATGCCGGGGTGTGCTGCCCGGGCAGGCC  
ATGTTGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGGAGCACAAG  
GCCCCGGTAGTGAAGGAACCCCCGTCTCCTGAGAGTGGGGCTGACCTGCCTTGGGCGC  
CGAGGGGTGGGGGGTGGGTGTGGGGGAGCCGTTAGGCCTCCAGGTCTTAGGATCAGG  
GTTGCCCCCAGAACCCCTTCCCATATCCTCCATTCTCCGCCCTGAGTTCCTACCCAGGCT  
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCAGC  
TCTGGGGCTTGGGGGTGAGGGTCAAGCCTGGACAGACCTCTGCCAGGGAACCTGCTCCAT  
GGGGTCTGGGAGAGCAGCCATCCCCTGCTGGCACCATAGACCCACACAAGGAGCCTGCAC  
AGCAAGCCAGCGGTGACACACCTGCAGGTGTGAGGCATGGCACTGGGCACAACAGGGACC  
TGGCAGGAGAAACAGACCACAGAGAGGTCTGGAGTTGAGGCTGTTGTGAGCAAGGCCCT  
GGTCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCCTTTACCCACCCCTGAGACCAG  
AAGTTGCAGCCCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCCCTCAATGGGCTTTTTC  
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCACATCCTCCCTGCTCCTCAGAC  
TCACAGCCCCCTCCATGTTACCTCCCGCACCTCCTCCCTGGGGCAGCTGCTCCCTGGGCCCT  
CTGAGGATGTCAGCTCCTGGCTCCCTGCCTCTCTCCCACTCCACTCCTGCTCAGTCTTA  
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCTGGCCTCTTGATTCTTGGCTT  
GCCTCTCCTCCAATTCCAACTTAGTGAAATGGCCTTAAGCATTTTAAACTGTATGTATA  
CATTAGCGCATTCATGCCTTTCTAAACGCATTTCAATGTCAACCAGGAAGGCACACCAC

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FIGURE 2WW

TGTATTAGTTTTATACTGCCGCTGTAAAATTTACCACAAACCTTAGTGACTTAACACAAAT  
TTATTGCAATTCTGTAGGCTGGAAGTCTGACTATGGGTCTCACTGGACTAGAATCAAGGC  
TGGCAGGCTGCCTTCCTTCCTGGAGGTTCTAGGGGAGACTCTGTCTCCTGCTCCTTCAGG  
CTGCTGGCAGAATCAGATCCTTTTCGGTGGCAGGGCCAAGTCCGCACTTTCTTGCTGAC  
TGTAACCTAAGGCCACTTCCAGCTTGTAGAGGCTGCCTACATTCCCTTGGCTCCTTGGCCCC  
CTCCTCCATCTTCAGAGCTAGCAGGTTTCTGTGTGTACGAACCAATTTCTCTGGTTCCC  
TGCAGACAGGAAAGGTTGTCCCTAAGGACTCATGAGATTAGGTTGGGCCCAGCCAGATAA  
TACATGATAATCTCCCTCCTCAAGGTTTTTAATATTAAACACATCTGCAGGACACATTTT  
GCCATGTAACTAACATTCACTGGTTCCAGGGATTAAGGAATGAACCTCTTTGTTGGGG  
AAGGTTGGCATTCTGCTGACCACAGCACTCCAACCAAAAGCCAAAACCAAGCAAGACT  
TACTAACGCATATCAAATAAATTAAAGGTACAAAATCGTGAATCTCAGTTATCTTAAATA  
TTCCAATACTATTTACAAAATTATTCAAATTTCTCAGCCTTCCAACCTCAAATTAGCAAT  
CTAAAGTAATTTCCATATCCTAGATGGAAACCCTCATGCTAAACTGTCTGATTATGCATG  
GTTCTAAATGGTTTCAGTGGCAAATACATAACATTGTACTACTGATTAACTGAACTTAA  
AAGC

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CCACGCGTCCGCACCAGAGTATGGCGAAGTCAATGATGGGACTGGCTTTGTGGACATCTT  
CTCCTTCGGGATGTGTGCACTGGAGATGGCTGTACTCGAGATCCAAGCCAACGGGGATAC  
CAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGGCACTCACTGAGTGACCCCAACATGCG  
GGAATTCATCCTCTCCTGCCTGGCCCCGGGACCCTGCCCGCCGACCCTCAGCCCACAACCT  
CCTCTTCCACCGAGTGCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTT  
CATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTAGAGGAAAAGACCAAGGCCATGGA  
CCTCCATGCAGTTTTTGGCTGAGATGCCGAGCCCCATGGACCCCCAATGCAGTGGCGGTA  
CTCAGAGGTCTCCTTCTTGGAGCTGGACAAATTCCTAGAGGATGTGAGGAACGGGATCTA  
TCCACTGATGAACCTTTGCGGCTGCTCGGCCCTTGGGGCTTCCCCGTGTGTGGCCCCACC  
CCCAGAGGAAGCCCCAAAAGGCCAAAACCTCCAACGCCAGAACCCTTTGACTCGGAGACCAG  
GAAGGTGGTCCAGATGCAGTGCAACCTGGAAAGAAGCGAGGACAAGGCTCGGTGGCACCT  
TACTCTGCTCTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCC  
AACGGACAGTGCCCAAGGACCTCGCTGCTGAACCTAGTGCAATTATGGCTTCTGACAGGGA  
TGACAGGACAAAGCTAGCAGCCTTTCTGGAGACCACTTTCTCAAGTACCGAGGGACGCA  
AGCGTGACCTTCCCAGTCTGACGGCCAGCAGAGATACAGGGGCTCAGGGTTGTCCACT  
TGGCAAAGAGCCCCCACTGCTCAAAGCTGCCTTCTGCCTGTGTTCCCTGGAACCTGAAC  
ACAGGCCCTGCTAGTGAAGACACCCCCACCCCCAGCTTTCTGCAGCAGTGTGGGACCCT  
GGGGTGGTGATGGAGCCCTGAGCCTGGACGAGAGTGGATACAGGTGAGTTAGGGGAACCG  
CTCCATCTGGTACTAGACAACAGCCATGCCTTCAGGTGGCATAGAAACCTAGGGAAGGAG  
CCTGAACTCAGGTGTACAGTGCTGGGCATCAGGCAGACCAGACCTGACCTGATTGGAGA  
ACTGTAGACTAGATAGCTTGGAGTTGAACCCATGGCCAGGGAAATTCCTTGGTCTGCTCA  
GACCAGTCTGATCCCTTGCAGACCTGCCTTGAACCTCTTTCTGATCTTCCACACTCTT  
GAGACCAGGACCTGTGTCTCCCCAAAGCCCTTGGGAAGGATCTTTCTATTATCATCCC  
TCTGGCCTAGGGGCTCAGGGGTGAGGCATCCTCCACATTCCCTCCCTGGGGAAGTTGTGT  
GTTTGAGTTGAGGATGTGGGTTCTTGGCTCCCTCTTTCTCCCCAGCCCCAACTTGTCTCTT  
TCTTACTGGTTTCAAAGTCTGATGAACGCTTCCCCTCAGAGCCACCCTGGTTTCTTGG  
TTCTTGAACCTGCCTCTCTCCCAACTTCAAACCAGGTCTTAAACGTTTTTAAATGCATAT  
ATAAATGTAATGCAGTCACGGTCTTTTTTAAACACTTTGTGTATGAAACCAGGAAAGCTC  
ACTATTGTATTAGGAATAGTTCCACATTGCTGCTGTAAACAGATATCATAAACCAGTGG  
TTTGAGACGACACACACACACACACACACACACAGAGAGAGAGAGTCTGTGA  
CATCAAGTGTGATCCAGGCTCTCACTAGATTAATACCCAGGCTAAGTTCTTCTGGAAG  
CTGGGACTTACCTCCTGCTCCTTCAAGCTATTGGCAGAACTCACTTCCCTGCAATGGTAA  
GGCAGAAATCCCTATTTTCTCAACAGCTGCCAACTAAGAACCCTCTCAGCTTCTAGAGG

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## FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT  
CTTTGTCCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA  
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCTTCTCAGGGTCTATAGATGAAC  
CACACCTGCGCAGTTCCTTCTGCTGTCATCCTGGGCTTTGGTGCTTGGAGAACAGCCGTG  
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA  
AATAAACAGATTTGTCATGGGACATCTAATAAATTAAATGAACTCTG

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CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCGACCATGTCTGGCGGCGCCGCGAG  
AGAAGCAGAGCAGCACTCCCGGTTCCCTGTTCTCTCGCCGCGGCTCCTGCCCCCAAGA  
ACGGCTCCAGCTCCGATTCCTCCGTGGGGGAGAACTGGGAGCCGCGGCCGCGGACGCTG  
TGACCGGCAGGACCGAGGAGTACAGGCGCCGCCACACTATGGACAAGGACAGCCGTG  
GGGCGGCGCGACCACTACCACCACTGAGCACCCTTCTTCCGCGGAGCGTCTCTGCG  
ACTCCAATGCCACTGCACTGGAGCTTCCCGGCTTCTCTTCCCTGCCCCAGCCAGCA  
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGAAGAGACCGTGACCG  
CCACCGCCACTTCCCAGGTAGCCAGCAGCCTCCAGCCGCTGCCGCCCCCTGGGGAACAGG  
CCGTCGCGGGCCCTGCCCCCTCGACTGTCCCCAGCAGTACCAGCAAAGACCGCCAGTGT  
CCAGCCTAGCCTTGTGGGGAGCAAAGAGGAGCCGCGCGCGGAGAAAGTGGCAGCGGCG  
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC  
TGGAGACCAAGGCCGTGGGAATGTCTAACGATGGCCGCTTTCTCAAGTTTGACATCGAAA  
TCGCCTGGTGTGAACTGCAGGATCGAAAAATTAACAAAGTCTGAGAGGCAGAGATTTAAAG  
AAGAAGCTGAAATGTTAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCTT  
GGGAATCCACAGTAAAAGGAAAGAAGTGCAATTGTTTTGGTGACTGAACTTATGACGTCTG  
GAACACTTAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT  
GGTGCCGTGAGATCCTTAAAGGTCTTCAGTTTCTTCATACTCGAACTCCACTTATCATTC  
ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG  
GAGACCTCGGTCTGGCAACCCTGAAGCGGGCTTCTTTTGCCAAGAGTGTGATAGGTACCC  
CAGAGTTTATGGCCCCCTGAGATGTATGAGGAGAAATATGATGAATCCGTTGACGTTTATG  
CTTTTGGGATGTGCATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA  
ATGCTGCGCAGATCTACCGTCGCGTGACCAGTGCGGTGAAGCCAGCCAGTTTGTGACAAAG  
TAGCAATTCCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAACAAAGATGAAA  
GATATTCATCAAAGACCTTTTGAACCATGCCTTCTTCCAAGAGGAAACAGGAGTACGGG  
TAGAATTAGCAGAAGAAGATGATGGAGAAAAAATAGCCATAAAATTATGGCTACGTATTG  
AAGATATTAAGAAATTAAGGGAAAAATACAAAGATAATGAAGCTATTGAGTTTTGTTTTG  
ATTTAGAGAGAGATGTCCCAGAAGATGTGACACAAGAAATGGTAGAGTCTGGGTATGTCT  
GTGAAGGTGATCACAAGACCATGGCTAAAGCTATCAAAGACAGAGTATCATTAATTAAGA  
GGAAACGAGAGCAGCGGCAGTTGGTACGGGAGGAGCAAGAAAAAAGCAGGAAGAGA  
GCAGTCTCAAACAGCAGGTAGAACAATCCAGTGCTTCCAGACAGGAATCAAGCAGCTCC  
CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCAGCTTCAGTTTCTACACAAG  
TAGAACCTGAAGAACCTGAGGCAGATCAACATCAACAACCTACAGTACCAGCAACCCAGTA  
TATCTGTGTTATCTGATGGGACGGTTGACAGTGGTCAGGGATCCTCTGTCTTACAGAAT  
CTCGAGTGAGCAGCCAACAGACAGTTTCATATGGGTTCCCAANNCATGAACAGGCACATT  
CTACAGGCACAGTCCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG  
GGGTATATCCACCCCTCAAGTGTGCAGCAGGGAATACAGCAGACAGCCCCTCCTCAACAGA  
CAGTGACAGTATTCATTTACAGACATCAACCTCCAGTGAGGCCACTACTGCACAGCCAG  
TGAGTACAGCCTCAAGCTCCACAAGTCTTGCCTCAAGTATCAGCTGGAAAACAGAGTACTC  
AGGGAGTCTCTCAGGTTGCTCCTGACAGAGCCAGTTGCAGTAGCACAGCCCCAAGCTACCC  
AGCCGACCACTTTGGCTTCTCTGTAGACAGTGCACATTGAGTGTGCTTCAGGTATGA  
GTGATGGCAATGAGAACGTCCCATCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

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## FIGURE 2YY

GGCATTACCGAAAAATCTGTAAGGAGTCGCTCTCGACATGAAAAAACTTCACGCCCAAAAT  
TAAGAATTTTGAATGTTTCAAATAAAGGAGACCGAGTAGTAGAATGTCAATTAGAGACTC  
ATAATAGGAAAAATGGTTACATTCAAATTTGACCTAGATGGTGACAACCCCGAGGAGATAG  
CAACAATTATGGTGAACAATGACTTTATTCTAGCAATAGAGAGAGAGAGTCGTTTGTGGATC  
AAGTGCGAGAAAAATTATTGAAAAAGCTGATGAAATGCTCAGTGAGGATGTGAGTGTGGAAC  
CAGAGGGTGATCAGGGATTGGAGAGTCTACAAGGAAAGGATGACTATGGCTTTTTCAGGTT  
CTCAGAAATTGGAAGGAGAGTTCAAACAACCAATTCCTGCGTCTTCCATGCCACAGCAAA  
TAGGCATTCCTACCAGTTCTTTAACTCAAGTTGTTTCACTTCTGCGGGAAGGCGGTTTATAG  
TGAGTCCTGTGCCAGAAAGCCGATTACGAGAATCAAAAAGTTTCCCCAGTGAAATAACAG  
ATACAGTTGCTGCCTCTACAGCTCAGAGCCCTGGAATGAACTTGTCTCACTCTGCATCAT  
CCCTTAGTCTACAACAGGCCCTTTTCTGAACTTAGACGTGCCCAAATGACAGAAGGACCCA  
ATACAGCACCTCCAAACTTTAGTCATACAGGACCAACATTTCCAGTAGTACCTCCTTTCT  
TAAGTAGCATTGCTGGAGTCCCAACCACAGCAGCAGCCACAGCACCAGTCCCTGCAACAA  
GCAGCCCTCCTAATGACATTTCCACATCAGTAATTCAGTCTGAGGTTACAGTGCCCACTG  
AAGAGGGGATTGCTGGAGTTGCCACCAGCACAGGTGTGGTAACTTCAGGTGGTCTCCCCA  
TACCACCTGTGTCTGAATCACCAGTACTTTCCAGCGTAGTTTCAAGTATCACAATACCTG  
CAGTTGTCTCAATATCTACTACATCCCCGTCACCTCAAGTCCCCACATCCACATCTGAGA  
TCGTTGTTTCTAGTACAGCACTGTATCCTTCAGTAACAGTTTCAGCAACTTCAGCCTCTG  
CAGGGGGCAGTACTGCTACCCCAAGTCCCTAAGCCTCCAGCTGTAGTATCTCAGCAGGCAG  
CAGGCAGCACTACTGTGGGAGCCACATTAACATCAGTTTCTACCACCACTTCATTCCCAA  
GCACAGCTTCACAGCTGTCCATTACAGCTTAGCAGCAGTACTTCTACTCCTACTTTAGCTG  
AAACCGTGGTAGTTAGCGCACACTCACTAGATAAGACATCTCATAGCAGTACAACCTGGAT  
TGGCTTTCTCCCTCTCTGCACCATCTTCCTCTTCTCCTGAGCAGGAGTGTCTAGTT  
ATATTTCTCAGCCTGGTGGGCTGCATCCTTTGGTTCATTCCATCAGTGATAGCTTCTACTC  
CTATTCTTCCCCAAGCAGCAGGACCTACTTCTACACCTTTATTACCCCAAGTACCTAGTA  
TCCCACCCTTGGTACAGCCTGTTGCCAATGTGCCTGCTGTACAGCAGACACTAATTCATA  
GTCAGCCTCAACCAGCTTTGCTTCCCAACCAGCCCCATACTCATTGTCTGAGTAGATT  
CTGATACACAACCCAAAGCTCCTGGAATTGATGACATAAAGACTCTAGAAGAAAAGCTGC  
GGTCTCTGTTTCAGTGAACACAGCTCATCTGGAGCTCAGCATGCCTCTGTCTCACTGGAGA  
CCTCACTAGTCATAGAGAGCACTGTACACCAGGCATCCCAACTACTGCTGTTGCACCAA  
GCAAACCTCCTGACTTCTACCACAAGTACTTGCTTACCACCAACCAATTTACCCTAGGAA  
CAGTTGCTTTGCCAGTTACACCAGTGGTTCACACCTGGGCAAGTTTCTACCCCAAGTCA  
CTACTACATCAGGAGTGAAACCTGGAAGTGTCTCCCTCCAAGCCACCTCTAAGGCTC  
CGGTGCTGCCAGTGGGTACTGAACTTCCAGCAGGTAAGTCTACCCAGCAGCAGCTGCCAC  
CTTTTCCAGGACCTTCTCTAACCAGTCCAGCAACCTCTAGAGGATCTTGATGCTCAAT  
TGAGAAGAACAACCTTAGTCCAGAGATGATCACAGTGAAGTCTGCGGTTGGTCTGTGTCCA  
TGGCGGCTCCAACAGCAATCACAGAAGCAGGAACACAGCCTCAGAAGGGTGTCTCTCAAG  
TCAAAGAAGGCCCTGTCTAGCAACTAGTTCAGGAGCTGGTGTCTTTTAAAGATGGGACGAT  
TTCAGGTTTCTGTTGCAGCAGACGGTGCCCAAGAGGGTAAAAATAAGTCAGAAGATG  
CAAAGTCTGTTCAATTTGAATCCAGCACCTCAGAGTCTCAGTGCTATCAAGTAGTAGTC  
CAGAGAGTACCTTGGTGAAACCAAGAGCCGAATGGCATAACCATCCCTGGTATCTCTTCAG  
ATGTGCCAGAGAGTGCCCAAAAACCTACTGCCTCAGAGGCAAAGTCAGACACTGGGCAGC  
CTACCAAGGTTGGACGTTTTTCAGGTGACAACTACAGCAAACAAAGTGGGTGCTTTCTCTG  
TATCAAAAACCTGAGGACAAGATCACTGACACAAAGAAAGAGGACAGTGGCATCTCCTC  
CTTTTATGGATTGGAACAAGCTGTTCTTCTGCTGTGATACCAAAGAAAGAGAAGCCTG  
AACTGTGAGAGCCTTCACATCTAAATGGGCCGTCTTCTGACCCGGAGGCCGCTTTTTTAA  
GTAGGGATGTGGATGATGGTTCCGGTAGTCCACACTCGCCCCATCAGCTGAGCTCAAAGA  
GCCTTCTAGCCAGAATCTAAGTCAAAGCCTTAGTAATTCATTTAACTCCTTACATGA  
GTAGCGACAATGAGTCAGATATCGAAGATGAAGACTTAAAGTTAGAGCTGCGACGACTAC  
GAGATAAACATCTCAAAGAGATTCAGGACCTGCAGAGTCGCCAGAAGCATGAAATTGAAT



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## FIGURE 2ZZ

CTTTGTATACCAAACCTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC  
TTTCAGGGGAGAAGACGACGACCCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT  
CCTTGGGGGAATAAAAGCCCCCAGCTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG  
TCTTGCACCCCCCAGCAGACCCTCCACCCTCCTGGCAACATCCCAGAGTCCGGGCAGAATC  
AGCTGTTACAGCCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTACGCCTTCACCA  
GTGATGGTGCCATTTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA  
TCATCGTCCAAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTTAAG  
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACTGAAGAATCTGG  
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA  
ATTACTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC  
TCATTTGGGATTTGGAACCTTAGGCTTTAATATTAGGCTGAGATTTCTGGATGAAATTCT  
AAGGTGTTTTAGCAGTTTCTGAAGCTAATACATTTTCTTAGCCATTGTAGAATTTTGTTA  
CTTTTAAGTATGGGAGTGGCATACTAAAATGAATAACCTTACAATTCAGTTTTTTATCCA  
TAATCTACTTTCCAAATATAGCTCTGTTTATTAGTGATTGCTGAAAAAATCCCACAGAG  
GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTTGGGCATCTGGGTGAGAA  
GAATGAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA  
GATCAGTCTCTTCACAGGAAGAATGCACCTTGATTGGTAAGGAGGGCAAACCTAGCTAGCAT  
TATTCGAACTAAGAAAAGCTTCCGCATTTTGCAGATGGGTAGAATTAAGACCTAATATTT  
CATCTCTTACATATCTGACCTTCCCCCAGAAGCTTGTTCTTCTGTGTGCCATCTTAGTG  
CATTTACCACTCCAGCCTCAAGTTTCTAACATCTTGTAGTTGTGTTCTGTCTCTTCTCC  
TCTCTCTGTTCTACCTGTTTTTCCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC  
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTTCTGAGTACGCCCTGCTT  
GGCTCTTTGTGTGTAAACACCTTTACTCCTTCTTGTCTTGTGTTTCTGCTGCTTGGATC  
TGATGTTTCACGCAGTCCATTTTCATTGTCTCTTTTGTATATCATCTACTCAGTGGCT  
TGGCTGAATTACTGTTACCCTCAGAAGTTTGGGCCCCCACAATTAATTATGATAAAAAATG  
TCAAAATAACAAGTTATCTACAAATTTCAATGTAACTTTCTGGTAGAAGTGCTTCTTCAT  
GGATCTGTGACAGAGAGTGGATATGGTATCTAGGCAATAGATTGCTGGGTCAATTTAGAA  
AATGAAGACTGAACTCCACAGTCGTAGTCAGTGCTGTCTGTCTGCCCTAGCATTAGAAAT  
GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA  
GGCGGAAGATTGCTTGAGGCCAGGAGCTCGAGACCAACCCTGGGCAACATGGTGATACC  
CCATCTCT

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GCGGAGCGCAGCTGTGAGGGAGTCGCTGTGATCCGGGGCCCCGGAACCCGAGCTGGAGCT  
GAAGCGCAGGCTGCGGGGCGCGGAGTCGGGAGGCCTGAGTGTTCTTCCAGCATGTCGGA  
GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC  
AGCTCCTGGCCTGACATCAGTGTACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC  
AGAGGAAGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTGGAAAGAGTCGCCCTGTGGGCG  
CTGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA  
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGA  
ACGCAAGAACTACAAGCTGCAGGAGGAAAAGGTTCTGTGCTGTGTTTGATAATCTGATTCA  
ATTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACA  
GGCCAGGGTCATTTTTATCACAGAATACATGTCTGAGGAGTCTGAAGCAATTTCTGAA  
GAAGACCAAAAAGAACCAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGACACACA  
AATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCATCATCCATGGGAACCT  
GACCTGTGACACCATCTTCATCCAGCACAACGGACTCATCAAGATTGGCTCTGTGGCTCC  
TGACACTATCAACAATCATGTGAAGACTTGTGCGAGAAGAGCAGAAGAATCTACACTTCTT  
TGCACCAGAGTATGGAGAAGTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGG  
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTACGGGCAATGGAGAGTCCTCATATGT  
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCCATTACAGAGGGAGTT

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## FIGURE 2AAA

CATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTT  
CCACCCAGCATTGTTTGAAGTGCCCTCGCTCAAACCTCCTTGCGGCCCCACTGCATTGTGGG  
ACACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACCAAAAAACATGGATACTAG  
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTCAGACTTTGTACTC  
TCAGTCACCAGCTCTGGAATTAGATAAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC  
TCTGACAGCCTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC  
TGTCGTGCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA  
GGTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGGAGTCAAACACCACCTGAC  
ACTTCTGCTGAAGTTGGAGGACAAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA  
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA  
CCAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTGCCAGGAA  
CAGTACCCCTCAACTCAGCCGCTGTCAACGTCTCCTCTTAGAGCTCACTCGGGCCAGGCCC  
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCAGTC  
AGTATTACCCTGTGAAGCCCCCTTCCCTCCTTTATTATTTCAGGAGGGCTGGGGGGGCTCCC  
TGTTTCTGAGCATCATCCTTTCCCTTCCCTCTCTTCCCTCCTCTGCACTTTGTTTACT  
TGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCGCCTTCTAGTTGGGGGCTAGT  
CGCTGATCTGCCGGCTCCCGCCAGCCTGTGTGGAAAGGAGGCCACGGGCACTAGGGGA  
GCCGAATTCTACAATCCCGCTGGGGCGGCCGGGGCGGAGAGAAAGGTGGTGCTGCAGTG  
GTGGCCCTGGGGGGCCATTGATTGCTCAGTTGCTGCTGTAATAAAAGTCTACTTTTT  
GCT

SEQ ID NO: 65\_AA711829\_M

CTTAAGCAGTTTCTGAAGAAGACCAAAAGAACCACAAGACTATGAATGAAAAGGCTTGG  
AAACGCTGGTGTACACAGATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCTCCC  
ATCATCCATGGGAACCTGACCTGTGACACCATCTTCATCCAGCACAAACGGACTCATCAAG  
ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGGAAGAACAG  
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCACAAACGTGACAACAGCAGTG  
GACATCTACTCCTTTGGCATGTGTGCACTGGAGATGGCAGTGCTGGAGATTGAGGGCAAT  
GGCGAGTCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC  
TCATTACAGAGGGAGTTTATTCAAAGTGCCTGCAGTCTGAGCCTGCTCGGAGACCAACA  
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCCTCACTCAAGCTTCTTGCT  
GCTCACTGTATCGTGGGGCACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACC  
AAGAACATGGATAACAGTGCTGTACTAGCTGAAATTCCCGCAGGGCCAGGACGAGAACCA  
GTTGAGACTTTGTACTCTCAGTCACCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC  
AGGAATGGGATCTACCCCTTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG  
GAGGAGGTGACATCACCTGTTGTGCCCCCTCTGTCAAGACTCCAACCTCCTGAGCCAGCT  
GAAGTGGAGACACGAAAGGTGGTGCTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA  
GTCAAACACCATCTAACACTTCTGCTGAAGCTGGAGGACAAATTGAACCGGCACCTGAGC  
TGTGACCTGATGCCAAATGAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGACGCTGGGC  
TTCATTAGTGAGGCTGATCAGAGCCGCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG  
TTCAACTTCACCAGGAACAGTACACTCAACACAGCCACTGTACCGTCTCCTCGTAGAGC  
TCACTTGAGCCAGGCCCTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCAGTCTCCTCT  
GTCCCTTCTCCCCAGTCAGTATTACCCTTCGCGCCCATATTATTAGGAGGGCTTTAGGG  
GCTCCCTGGTTGAGTATCACCTGCCCCCTTCCCTCTCTTCCCTCCTCTGCACTTTGTT  
TACTTGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCACCTTCTAGCTGGGGGC  
TAGTAGCTGACCTGCTGCCCTCCTGCCCTACTTGTGTGGACAGGAGGCCACGGGCACTGG  
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGCTGCA  
GGGGTGGCCCCCGGGGGGGCATTGGAATCACCTCAGTTGCTGCTGTAATAAAGTCTAC  
TTTTTGCT

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## FIGURE 2BBB

SEQ ID NO: 66\_AA099102\_H

ATGTCATCATGTGTCTCTAGCCAGCCCAGCAGCAACCGGGCCGCCCCCAGGATGAGCTG  
GGGGGCAGGGGCAGCAGCAGCAGCGAAAGCCAGAAGCCCTGTGAGGCCCTGCGGGGCCTC  
TCATCCCTTGAGCATCCACCTGGGCATGGAGTCCTTCATTGTGGTTCACCGAGTGTGAGCCG  
GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGGCCCTGGAGGCCGATGGCCAAGAG  
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCGGCCCCACCTCTCCGGTCGCAAGCTGTCT  
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGGACGC  
TGCATCTGCCCCGTCCCTGCCCTACTCACCCTGTCAGCTCCCCGCAGTCTCGCCTCGGCTG  
CCCCGGCGGCCGACAGTGGAGTCTCACCACGTCTCCATCACGGGTATGCAGGACTGTGTG  
CAGCTGAATCAGTATACCTGAAGGATGAAATTGAAAGGGCTCCTATGGTGTCTGCAAG  
TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAAG  
CTGATCCGGCAGGCCGCTTTTCCACGTGCGCCCTCCACCCCGAGGCACCCGGCCAGTCTCT  
GGAGGCTGCATCCAGCCCAGGGGCCCATTTAGCAGGTGTACCAGGAAATTGCCATCCTC  
AAGAAGCTGGACCACCCCAATGTGGTGAAGCTGGTGGAGGTCTTGGATGACCCCAATGAG  
GACCATCTGTACATGGTGTTCGAACTGGTCAACCAAGGGCCCGTGATGGAAGTGCCACC  
CTCAAACCACTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC  
GAGTACTTACACTACCAGAAGATCATCCACCGTGACATCAAACCTTCCAACCTCCTGGTC  
GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAAGGGCAGT  
GACGCGCTCCTCTCCAACCTACGTGGGCACGCCCGCCTTCATGGCTCCCGAGTCGCTCTCT  
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA  
TACTGCTTTGTCTTTGGCCAGTGCCCATTCATGGACGAGCGGATCATGTGTTTACACAGT  
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAG  
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGGTGGCCGAAATC  
AAGCTGCACCCCTGGGTACGAGGCATGGGGCGGAGCCGTTGCCGTGCGAGGATGAGAAC  
TGCACGCTGGTTCGAAGTGACTGAAGAGGAGGTGAGAACTCAGTCAAACACATTCCCAGC  
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTC  
GAGGGCAGCCGGCGGGAGGAACGCTCACTGTGAGCGCCTGGAACTTGCTCACCAAAAAA  
CCAAGCAGGGAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAGCGAAGACAACCT  
CCAGGGCACCGACCCGCCCCCGTGGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC  
TGCGTGGAAAGTTGCTGGGCCCCCGCCCCGGCTCCCCCGCACGCATGCATCCACTGCGG  
CCGGAGGAGGCCATGGAGCCCGAGTAG

SEQ ID NO: 67\_5R69\_17\_2\_H

CCGGGATGTGAGCCTGGTGGTTGGCAGCTGGAGCCACGTGCGAGGGGGAAGTGTGCGAGC  
ATTCTCTGCAGGCATCACAGACCTGAGGCAGTGGCCTCCGGAGGGCACTGGACAGAAACA  
GCCATCCAAGTGGCTGAGTGGAGGGACCCTGCTCAAGTGCAGCTGCAGTGGCCGGGGTTT  
CCCTCAGGTAGGGATCGGGGCGCCTTGTGCGCCGACCCAGTGTGGCGTCCGGTACAGT  
CAGCAGAGTGCAGGGTGCGGGCACCAGGAAAGGGGGCGCAGGGGAACTCCCGCGGGCCTC  
GCGTTTGGAACTTCTCGCCTGGGCAGGAGGCGGTGCTGGGAAAGAAGGTGGAAGAGCGA  
GCTTTTTGGAACTGTGCACGGGACAGATTGGACGCACACCCCTCGGGAGGCGCGAAGGCA  
TGGAATAATTGAAGCATATTATCACCCCTGGCCAGGTCTCCACAAACGGTGTGAAGAGA  
TGAAATACTGCAAGAAACAGTGCCGGCGCCTGGGCCACCGCGTCTCGGCCTGATCAAGC  
CTCTGGAGATGCTCCAGGACCAAGGAAAGAGGAGCGTGCCCTCTGAGAAGTTAACCACAG  
CCATGAACCGCTTCAAGGCTGCCCTGGAGGAGGCTAATGGGGAGATAGAAAAGTTACAGCA  
ATAGATCCAATATCTGCAGGTTTCTAACAGCAAGCCAGGACAAAATACTCTTCAAGGACG  
TGAACAGGAAGCTGAGTGATGTCTGGAAGGAGCTCTCGCTGTTACTTCAGGTTGAGCAAC  
GCATGCCTGTTTTACCCATAAGCCAAGGAGCGTCTGGGCACAGGAAGATCAGCAGGATG  
CAGACGAAGACAGGCGAGCTTTCCAGATGCTAAGAAGAGATAATGAAAAATAGAAGCTT  
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAAACTTTGAGGCAGTGTAAGT  
TATCATGTGCCCTGCTGTTTCTGATGGCCCCCAAAGTAGAAGTCATCAGTTTACTGGGAC

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## FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC  
CACAGGTTTGGGGATCCATTTCATGGCTAGCCAGGCTTCTGTCCATGGAATAACATGTGG  
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT  
ATGAATAGAATCAAAGCTTCAGTTTCAGTTGCTGAATTTCCAAGAAGAAATTCAAATCAA  
TTTAAATGCCACTCATTTCATTTCATCAACAAACTGTGAGTATCTGGTTTATGCCAGA  
GGCCATGCAAAGAGGTAAGTATGACAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG  
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG  
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC  
CAAGCTCTGGGTAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG  
GGTTAAGGCTGGAGGGACAGGCGGATTTGAAGAGGAGGAAAGGAAGTGGATGACACAT  
TCTGTCTAAGTGTCCAGCTGTGTCTTACTGGTCACTCAGAGGCACGGGAGCCGCTCCCTT  
GGGCTGAGTCCATCAGAAGCCCCAGCCACCAGCTCTGGTTTCATGTAGTAGAGCTTCC  
CACTCACACATCACAATATGCCACCTCCCTTAGGACCCCTTCTCTGCTCATTGACTCT  
TTTGTCTTCTTCTCTCGGGGGTGAGGTTCAGATTTACCACCAAATATGCAGGAGAT  
CCCGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT  
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATACCACAGAGCTCCAGTGGC  
CATAAAGTATTCAAAAACTCCAGGCTGGCAGCATTGCAATAGTGAGGCAGACTTTCAA  
TAAGGAGATCAAAACCATGAAGAAATTCGAATCTCCCAACATCCTGCGTATATTTGGGAT  
TTGCATTGATGAAACAGTGACTCCGCTCAATTCTCCATTGTTCATGGAGTACTGTGAAGT  
CGGGACCTGAGGGAGCTGTTGGATAGGGAAAAAGACCTCACACTTGGAAGCGCATGGT  
CCTAGTCTGGGGCAGCCCGAGGCTTATACCGGCTACACCATTTCAGAAGCACCTGAACT  
CCACGGAAAAATCAGAAGCTCAAACCTTCTGGTAACTCAAGGCTACCAAGTGAAGCTTGC  
AGGATTTGAGTTGAGGAAAACACAGACTTCCATGAGTTTGGGAACTACGAGAGAAAAGAC  
AGACAGAGTCAAATCTACAGCATATCTCTACCTCAGGAACTGGAAGATGTATTTTATCA  
ATATGATGTAAAGTCTGAAATATACAGCTTTGGAATCGTCTCTGGGAAATCGCCACTGG  
AGATATCCCGTTTCAAGGTGAAGAATGTGAAGACTGGCTCAGCCAGTGGCTGTAATTCTG  
AGAAGATCCGCAAGCTGGTGGCTGTGAAGCGGCAGCAGGAGCCACTGGGTGAAGACTGCC  
CTTCAGAGCTGCGGGAGATCATTGATGAGTGCCGGGCCCATGATCCCTCTGTGCGGCCCT  
CTGTGGATGAAATCTTAAAGAACTCTCCACCTTTTCTAAGTAGTGATCAAAATCTAAA  
CCAAGGAGTCTCTGGACAAGAAGCTGGGAGAGGCACGAAGTGGACATCTCTCTCTCAT  
ATCCTTCGGCATTTGGGTTATCTATGGGTGCAAGGAGTGGGCACGCTTCTCTGTTACAAAT  
AGAAAACGATTCAGTCATACAGGACACATCCCACTCCAAATGATATTTCCAAAAACATA  
CCTCTGACAGTAACCTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT  
CTTGGCAATGAAATTTGCAGCTCCTCCCTTCCATAAATGAAGTCTCTTTCCCCACCATT  
GAATCTGGGCTGGCACTGTGACTTGATTTGATCAATAGAATGTGGAAGAAGTGAAGTGTAT  
GCCAGTTCCAAGCCTAGGTTTCAAGAGGCCTTATAAATGTCTGTTGGAACCTTACCCAGC  
CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT  
TTCCTAGCTGAAGTCATACTAGCCCAACCAACATGGCAGCTAACACATGAATGAGGCCAA  
TCAAGACCAGAAGAACCACTCAAGCAGATCCCAGCCCAATTGCCCATTCACACAATCAG  
GAGCTAAATAAATTACTGTTGTCTTTT

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CGCCCCGGCCCCCTCCCCCGGCGCCGGCCACGGGAGGCGGTGATGCGGGCGCGGGCGGCCT  
CGGCTGCGCCGAGAGCGGAGACACAGGCTCAAGATGGCAGATTCCGACTGAGGCTGGGGG  
GGCCGAGCTCGCGCGCCGCTTTCCCGTCCCGTTGCCATGAACCGCGGACACCCCGGCC  
CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTTCTCCCTCACACCC  
TTCAATCAAGTGCCTTCTGTAGTGTGAAGAACTGAAAATAGAGCCGAGTTCCAAGTGGG  
ACATGACTGGGTACGGCTCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT  
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCCAAGCCTACCTT  
ACGAGCAGACCATCGTCTTCCAGGAAGCACCGGGCACATCGTGGTCACCTCAGCAAGCA

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FIGURE 2DDD

GCACCTTCTGT CACCGGGCAAGTCTCTCGGCGGACCACACAACCTAATGCGTTCGAAGCACTG  
TGAGCCTCCTTGATACCTACCAAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA  
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTAGAATAATGCAAGCG  
GGGCCACTGTGCGCCTGTCACCACGTCTACTGCCACCTCCAAAAACAGCGGCTCCAACA  
GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG  
AGGTCTTAGAGTTCTTGGGCCGAGGGACGTTTGGGCAAGTGGTCAAGTGCTGGAACGGG  
GCACCAATGAGATCGTAGCCATCAAGATCCTGAAGAACACCCATCCTATGCCGACAAG  
GTCAGATTGAAGTGAGCATCCTGGCCCGGTTGAGCACGGAGAGTGCCGATGACTATAACT  
TCGTCCGGGCCTACGAATGCTTCCAGCACAGAACCACACGTGCTTGGTCTTCGAGATGT  
TGGAGCAGAACCTCTATGACTTTCTGAAGCAAAACAAGTTTAGCCCCCTGCCCTCAAAT  
ACATTGCGCCAGTTCTCCAGCAGGTAGCCACAGCCCTGATGAAACTCAAAAGCCTAGGTC  
TTATCCACGCTGACCTCAAACCAGAGAACATCATGCTGGTGGATCCATCTAGACAACCAT  
ACAGAGTCAAGGTCATCGACTTTGGTTTCAGCCAGCCACGTCTCCAAGGCTGTGTGCTCCA  
CCTACTTGCAGTCCAGATATTACAGGGGCCCTGAGATCATCCTTGGTTTACCATTTTGTG  
AGGCAATTGACATGTGGTCCCTGGGCTGTGTTATTGCAGAAATTGTTCTGGGTTGGCCGT  
TATATCCAGGAGATTCCGAGTATGATCAGATTCCGGTATATTTCAAAACACAGGGTTTGC  
CTGCTGAATATTTATTAAGCGCCGGGACAAAGACAACCTAGGTTTTCAACCGTGACACGG  
ACTCACCATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGA  
TTAAGTCAAAAGAAGCAAGAAAGTACATTTTCAACTGTTTAGATGATATGGCCAGGTGA  
ACATGACGACAGATTTGGAAGGGAGCGACATGTTGGTAGAAAAGGCTGACCGCGGGAGT  
TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG  
AAACCCTGAACCATCCCTTTGTCAACCATGACACACTTACTCGATTTTCCCCACAGCACAC  
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA  
CGGTGAACCAGAGCAAAACCCCTTTCATCACGCACGTGGCCCCCAGCACGTCCACCAACC  
TGACCATGACCTTTAAACAACCAGCTGACCACTGTCCACAACCAGCCCTCAGCGGCATCCA  
TGGCTGCAGTGGCCAGCGGAGCATGCCCTGCAGACAGGAACAGCCCAGATTTGTGCCC  
GGCCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCGGCTTCCAAGGCTTGCAGG  
CCTCTCCCTCTAAGCAGCTGGCTACTCGGTGCGAATGGAAAATGCAGTTCCCATCGTCA  
CTCAAGCCCCAGGAGCTCAGCCTCTTCAGATCCAACCAGGTCTGCTTGCCCAGCAGGCTT  
GGCCAAGTGGGACCCAGCAGATCCTGCTTCCCCAGCATGGCAGCAACTGACTGGAGTGG  
CCACCCACACCTCAGTGCAGCATGCCACCGTGATTCCCGAGACCATGGCAGGCACCCAGC  
AGCTGGCGGACTGGAGAAATACGCATGCTCACGGAAGCCATTATAATCCCATCATGCAGC  
AGCCTGCACTATTGACCGGTCATGTGACCTTCCAGCAGCACAGCCCTTAAATGTGGGTG  
TGGCCACAGTATGCGGCAGCAGCCAACCAGCACCACTCCTCCCGGAAGAGTAAGCAGC  
ACCATCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCTCTCTCAGGCCATCAGCT  
CCCCAGCAGTCCAAGCGTGTCAAGGAGAACAACCTCCCCGCTGTGCCATGGTGCACA  
GTAGCCCGGCTGCAGCACCTCGGTACCTGTGGGTGGGGCGACGTGGCCTCCAGCACCA  
CCCGGGAACGGCAGCGGCAGACAATTGTCAATCCCCGACACTCCAGCCCCACGGTCAGCG  
TCATCAACCATCAGCAGTGACACGGACGAGGAGGAGGAACAGAAACACGCCCCACCAGCA  
CTGTCTCCAAGCAAAAGAAAAACGTATCAGCTGTGTACAGTCCACGACTCCCCCTACT  
CCGACTCCTCCAGCAACACCAGCCCCCTACTCCGTGCAGCAGCGTGCTGGGCACAACAATG  
CCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCA  
TCATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGG  
TGCCAGTCAACACCAAGTCAACCTCGTCTCTTACAAGTCCAAGTCTCCAGCAACGTGA  
CCTCCACCAGCGGTCACTCTTCAGGGAGCTCATCTGGAGCCATCACCTACCGGCAGCAGC  
GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA  
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCTACATCACTCCACCATG  
CCCAGGCTCCGTACTCCTTCCCGCACAACAGCCCCAGCCACGGCACTGTGCACCCGCATC  
TGGCTGCAGCCGCTGCCGCTGCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG  
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCACCTGGTGGCCTCGCAAGGCTCTG

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## FIGURE 2EEE

CGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCACCAGGTCCCCGTGA  
GCATGGGCCCCCGGTCTGCCCCTCGCCCACCATCCACCCGAGTCAGTATCCAGCCCAAT  
TTGCCACACAGACCTACATCAGCGCCTCGCCAGCCTCCACCGTCTACACTGGATAACCCAC  
TGAGCCCCGCAAGGTCAACCAGTACCCCTTACATATAAACACTGGAGGGGAGGGAGGGAG  
GGAGGGAGGGAGAGAATGGCCCCGAGGGAGGGAGGGAGAGAAGGAGGGAGGGCGCTCCTGGGA  
CCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAATGCAAACGGGGCAGG  
GGCGGGGGGGGGGGGGCAGAGGGCAGGGGGACGGGTCTGGGACACCAAGTGAACTTGAACC  
GGGAAGTGGGAGGACGTAGAGCAGAGAAGAGAACATTTTTTAAAGGAAGGGATTAAAGAG  
GGTGGGAAATCTATGGTTTTTTATTTTAAAAAAG

SEQ ID NO: 69\_DYRK3\_H

CGGGAGCGAAAGTGCCTGAGCTGCAGTGTCTGGTTCGAGAGTACCCGTGGGAGCGTCCGC  
CCGCGGAGGCAGCCGTCCCGGCGTAGGTGGCGTGGCCGACCGACCCCCAACTGGCGCCT  
CTCCCCGAGCGGGGTCCCGAGCTAGGAGATGGGAGGCACAGCTCGTGGGCCTGGGCGGAA  
GGATGCGGGGCGCCTGGGGCCGGGCTCCCGCCCCAGCAGCGGAGTTGGGGGATGGTGTG  
TATGACACCTTCATGATGATAGATGAAACCAAATGTCCCCCTGTTCAAATGTACTCTGC  
AATCCTTCTGAACACCTCCACCCAGAAGACTAAATATGACCGCTGAGCAGTTTACAGGA  
GATCATACTCAGCACTTTTGGATGGAGGTGAGATGAAGGTAGAACAGCTGTTTCAAGAA  
TTTGGCAACAGAAAATCCAATACTATTTCAGTCAGATGGCATCAGTGAAGTCTGAAAAATGC  
TCTCCTACTGTTTCTCAGGGTAAAAGTTTCAGATTGCTTGAATACAGTAAAATCCAACAGT  
TCATCCAAGGCACCCAAAGTGGTGCCTCTGACTCCAGAACAAGCCCTGAAGCAATATAAA  
CACCACCTCACTGCCTATGAGAACTGGAAATAATTAATTATCCAGAAATTTACTTTGTA  
GGTCCAAATGCCAAGAAAAGACATGGAGTTATTGGTGGTCCCAATAATGGAGGGTATGAT  
GATGCAGATGGGGCCTATATTCATGTACCTCGAGACCATCTAGCTTATCGATATGAGGTG  
CTGAAAATTATTGGCAAGGGGAGTTTTGGGCAGGTGGCCAGGGTCTATGATCACAACCTT  
CGACAGTACGTGGCCCTAAAAATGGTGCCTCAATGAGAAGCGCTTTCATCGTCAAGCAGCT  
GAGGAGATCCGGATTTTGGAGCATCTTAAGAAACAGGATAAACTGGTAGTATGAACGTT  
ATCCACATGCTGGAAAGTTTTCACATTCCGGAACCATGTTTGCATGGCCTTTGAATTGCTG  
AGCATAGACCTTTATGAGCTGATTAATAAAAAAATAAGTTTCAGGGTTTTAGCGTCCAGTTG  
GTACGCAAGTTTGGCCAGTCCATCTTGCAATCTTTGGATGCCCTCCACAAAAATAAGATT  
ATTCACTGCGATCTGAAGCCAGAAAACATTCTCCTGAAACACCACGGGCGCAGTTCAACC  
AAGGTCAATTGACTTTGGGTCCAGCTGTTTTCGAGTACCAGAAGCTCTACACATATATCCAG  
TCTCGGTTCTACAGAGCTCCAGAAATCATCTTAGGAAGCCGCTACAGCACACCAATTGAC  
ATATGGAGTTTTCGCTGCATCCTTGCAAGCTTTTAAACAGGACAGCCTCTCTCCCTGGA  
GAGGATGAAGGAGACCAGTTGGCCTGCATGATGGAGCTTCTAGGGATGCCACCACCAAAA  
CTTCTGGAGCAATCCAAACGTGCCAAGTACTTTATTAATTCCAAGGGCATAACCCGCTAC  
TGCTCTGTGACTACCCAGGCAGATGGGAGGGTTGTGCTTGTGGGGGGTCTGCTCACGTAGG  
GGTAAAAAGCGGGGTCCCCCAGGCAGCAAAGACTGGGGGACAGCACTGAAAGGGTGTGAT  
GACTACTTGTATTATAGAGTTCTTGAAAAGGTGTCTTCACTGGGACCCCTCTGCCCGCTTG  
ACCCAGCTCAAGCATTAAAGACACCTTGGATTAGCAAGTCTGTCCCCAGACCTCTCACC  
ACCATAGACAAGGTGTGAGGAAACGGGTAGTTAATCCTGCAAGTGCTTTCAGGGATTG  
GGTCTAAGCTGCCTCCAGTTGTTGGAATAGCCAATAAGCTTAAAGCTAACTTAATGTCA  
GAAACCAATGGTAGTATACCCCTATGCAGTGTATTGCCAAAACCTGATTAGCTAGTGGACA  
GAGATATGCCAGAGATGCATATGTGTATATTTTTATGATCTTACAAACCTGCAATGGA  
AAAAATGCAAGCCCATTTGGTGGATGTTTTTGTGTAGAGTAGACTTTTTTTTAAACAAGACAA  
AACATTTTTATATGATTATAAAGAATTCTTCAAGGGCTAATTACCTAACCAAGCTTGTAT  
TGGCCATCTGGAATATGCATTAAATGACTTTTTTATAGGTCA



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## FIGURE 2FFF

SEQ ID NO: 70\_AA589241\_M DYRK3\_M  
CCACGCGTCCGGAGTTGCTAGGAATGCCACCGCAGAACTTCTGGAGCAATCCAAGCGTG  
CCAAGTACTTTTATTAACCTCAAAGGCTTGCCCTCGATACTGCTCCGTATCTACCCAGACGG  
ACGGGAGGGTGGTGCTTCTCGGGGGTCTGCTCACGCAGGGGTAAAAAGCGAGGCCCGCCAG  
GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTTCATAGAGTTTC  
TGAAACGATGCCTCCAGTGGGACCCCTCTGCCCGCCTCACCCCGGCTCAAGCATTAAAGAC  
ATCCTTGGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC  
GGGTAGTTAAACCTACAAATGCTTTCCAGGGACTGGGTCCAAGCTGCCTCCAGTCTGTTG  
GGATAGCCAGTAAGCTTAAAGCTAACCTAATGTCCGAAACCAGTGGTAGTATACCTCTGT  
GCAGTGTATTGCCAAAGCTGATTAGCTAGTGACCACTCAGAGACTGATACATATCATAT  
GTATTTTAAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTAC  
TGATGGATATGTTTTTGTAGACTTTTTTTTAAACAAGGCAGAACATTTTTTATATGACTAT  
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT  
TAAATGACTTTTTTCATAGGTC

SEQ ID NO: 71\_5R72\_16\_2\_H  
GTCGAGGCGCAGCGCTGCCATGGCTGGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGA  
GCCTCCGGAGAGCTACCCGCAACGACAGGACCACGAGCTACAGGCCCTGGAGGCCATCTA  
CGGCGCGGACTTCCAAGACCTGCGGCCGGACGCTTGCGGACCGGTCAAAGAGCCCCCTGA  
AATCAATTTAGTTTTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGA  
TTTGAGGGTTAAATGCCACCTACCTATCCAGATGTAGTTCTGAAATAGAGTTAAAAA  
TGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAATCTCGCCTAGAAGAACTGGC  
CAAGAAACACTGTGGGAGGTGATGATCTTTGAACTGGCTTACCAGTGCAGTCATTTCT  
CAGCGAGCATAACAAGCCCCCTCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC  
TCAGGAGGAGCAGCAGAGGCTGTTGGAGGCCAAGCGGAAAGAAGAGCAGGAGCAACGTGA  
AATCCTGCATGAGATTCAGAGAAGGAAAGAAGAGATAAAAGAAGAGAAAAAAGGAAAGA  
AATGGCTAAGCAGGAACGTTTGGAAATGCTAGTTTGTCAAACCAAGATCATACCTCTAA  
GAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGT  
AGGAAATGGTAAACATCGGGCAAACCTCCTCAGGAAGGTCTAGGCGAGAAGCACTGATTC  
TGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATCTGTATTTCAATATGGGGAG  
TCCTGATCAGCTCATGGTGCACAAAGGGAATGTATTGGCAGTGTATGAACAACCTGGAAA  
ATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTATGAGTGGGT  
CCTTCAGTGGCAGAAAAAATGGGTCCATTCTTACCAGTCAAGAAAAAGAGAAGATTGA  
TAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAATTTAG  
CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT  
GGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTC  
AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTGAGCCCTTGA  
TTATCTGCACAGCAATTCTGTGGTGCATAAGGTCTGAGTGCATCTAATGTCTTGGTGGA  
TGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTG  
CAAGGAGGATGTGTTTGGAGCAAACCCGAGTTCTGTTTGTGACAATGCTCTGCCTTATAA  
AACGGGGAAGAAAGGAGATGTTTGGCGTCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGG  
ACAGGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGAATTTCTAAGCGCCTCGCAGACATTTG  
TTTTCTAAAGAAATGTGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT  
GAAACACAGCTTTATAAATCCCCAGCCAAAATGCCTCTAGTGGAAACAAAGTCTGAAGA  
TTCTGGAGGACAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGC  
CTTCTTTAGTGAGACACAGAGACAGTTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA  
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCTCAAGGTGCAGAACAAAGTTGGACGGCTG  
CTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAA  
GGGCGAAGTGACACTGCTGTACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC  
CTGGATCGAGCGGCACGAGCGGCCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCC

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## FIGURE 2GGG

CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA  
CAGCGTAGAGGCCCGCCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC  
GGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGA  
GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCTCAGTCTTCCTGCCTGCTTCAGA  
TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGA  
TGAAGATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGC  
TGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGAGACACCAT  
TGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTTCGAGAGATTCTGGA  
TGGATTAGCTTATATCCATGAGAAAGGAATGATTACCCGGGATTTGAAGCCTGTCAACAT  
TTTTTTGGATTCTGATGACCATGTGAAAATAGGTGATTTTGGTTTGGCGACAGACCATCT  
AGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCC  
TTCAGGTCACCTAACTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG  
AAGCACCAAATCTGCATACAACCAGAAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTT  
TGAGATGTCTTATCACCCCATGGTCACGGCTTCAGAAAGGATCTTTGTTCTCAACCAACT  
CAGAGATCCCACCTCGCCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCA  
GAAATCAGTCATCTCCTGGCTGTTGAACCACGATCCAGCAAAACGGCCCCACAGCCACAGA  
GCTGCTCAAGAGTGAGCTGCTGCCCCCACCACAGATGGAGGAGTCAGAGCTGCATGAAGT  
GCTGCACCACACGCTGACCAACGTGGATGGGAAGGCCTACCGCACCATGATGGCCCAGAT  
CTTCTCGCAGCGCATCTCCCTGCCATCGATTACACCTATGACAGCGACATACTGAAGGG  
CAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCAT  
CTTTAAAGACATGGAGCTGTTCACTGTGTACTCCACTACTGCTTCCCCGAAACAGACA  
AATATATGAGCACAACGAAGCTGCCCTATTTCATGGACCACAGCGGGATGCTGGTGTGCT  
TCCTTTTGACCTGCGGATCCCTTTTGCAAGATATGTGGCAAGAAATAATATATTGAATTT  
AAAACGATACTGCATAGAACGTGTGTTTCAAGCCGCGCAAGTTAGATCGATTTTCATCCCAA  
AGAACTTCTGGAGTGTGCATTTGATATTGTCACTTCTACCACCAACAGCTTTCTGCCCCAC  
TGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAG  
AAATTACAGTATTTATTTGAACCATAACCATGTTATTGAAAGCAATACTCTTACACTGTGG  
GATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAA  
GCTGACGAGGAGAGAAGTGGAAGCTAAATTTTGTAACTCTGTCTTTGTCTTCTAATAGTCT  
GTGTGCACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAAT  
AAATTCAATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGA  
CCTAGAGGAGGTTGTTGGACTGTTGAAGAACTCGGCATCAAGTTACAGGTCTTGATCAA  
TTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTT  
CATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACCT  
GCTGATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCATTGGGGT  
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCTCAACATGGAGGAATCTGTTACAAT  
AAGCTCTTGTGACCTCCTGGTTGTAAGTGTGGTCAGATGTCTATGTCCAGGGCCATCAA  
CCTAACCAGAAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACA  
GTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGT  
CTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGGAAAGGCAGACAGA  
GAAGCGTGTGCTGGAGACTGAACTTGTGGACCATGTACTGCAGAACTGAGGACTAAAGT  
CACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAGTGCAAAATCTGAAGGG  
GTCATTTTCTAATGCTTCAGGTTTGTGTTGAAATCCATGGAGCAACAGTGGTTCCTATTGT  
GAGTGTGCTAGCCCCGGAGAAGCTGTGAGCCAGCACTAGGAGGCGCTATGAAACTCAGGT  
ACAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAGCAGTGAAATTGAAAT  
TCTGGCTGTGGATCTACCCAAAGAAACAATATTACAGTTTTTATCATTAGAGTGGGATGC  
TGATGAACAGGCATTTAACACAACGTGTAAGCAGCTGCTGTACGCCTGCCAAAGCAAAG  
ATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAGGTGTCTGT  
GCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCCTAAAGAAC  
TGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTACAT



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## FIGURE 2HHH

TCATCATAATTTAAAATTAAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA  
 TCCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAG  
 CCT

SEQ ID NO: 73\_R43524\_H, HRI\_H  
 ATGCTGGGGGGCAACTCCGGGGTCCGCAAGCGCGAAGAGGAGGGCGACGGGGCTGGGGCT  
 GTGGCTGCGCCGCGGCCATCGACTTTCCCGCCGAGGGCCCGACCCCGAATATGACGAA  
 TCTGATGTTCCAGCAGAAATCCAGGTGTTAAAAGAACCCCTACAACAGCCAACTTCCCT  
 TTTGCAGTTGCAAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGCAT  
 GAACCAAACCCACTTCGTTCAAGACAGGTGTTAAGCTACTTTGCCAGACGTTTATCAAA  
 ATGGGGCTGTTGTCTTCTTCACTTGTAGTGACGAGTTTAGCTCATTGAGACTACATCAC  
 AACAGAGCTATTACACACTTAATGAGGTCTGTAAAGAGAGAGTTCGTCAGGATCCTTGT  
 GAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAGCCTTGGAAGCACAACCT  
 TCACGTTACTTAAATGAATTTGAAGAACTTGTCTATCTTAGGAAAAGGTGGATACGGAAGA  
 GTATACAAGGTGAGGAATAAATTAGATGGTCAGTATTATGCAATAAAAAAATCCTGATT  
 AAGGGTGCAACTAAAACAGTTTGCATGAAGGTCTACGGGAAGTGAAGGTGCTGGCAGGT  
 CTTACGACCCCAATATTGTTGGCTATCACACCGCTGGATAGAACATGTTTATGTGATT  
 CAGCCACGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTGGAAGTGCTCTCCGACCAG  
 GAAGAGGACAGAGAGCAATGTGGTGTAAAAATGATGAAAGTAGCAGCTCATCCATTATC  
 TTTGCTGAGCCCAACCCAGAAAAAGAAAAACGCTTTGGAGAATCTGACACTGAAAATCAG  
 AATAACAAGTCCGTGAAGTACACCACCAATTTAGTCATAAGAGAATCTGGTGAACCTTGAG  
 TCGACCCTGGAGCTCCAGGAAAATGGCTTGGCTGGTTTGTCTGCCAGTTCAATTGTGGAA  
 CAGCAGCTGCCACTCAGGCGTAATCCACCTAGAGGAGAGTTTACATCCACCGAAGAA  
 TCTTCCGAAGAAAATGTCAACTTTTTGGGTGAGACAGAGGCACAGTACCACCTGATGCTG  
 CACATCCAGATGCAGCTGTGTGAGCTCTCGCTGTGGGATTGGATAGTCGAGAGAAAACAG  
 CGGGGCGGGGAGTATGTGGACGAGTCTGCCTGTCTTATGTTATGGCCAATGTTGCAACA  
 AAAATTTTTCAAGAATTGGTAGAAGGTGTGTTTTACATACATAACATGGGAATTGTGCAC  
 CGAGATCTGAAGCCAAGAAATATTTTTCTTTCATGGCCCTGATCAGCAAGTAAAAATAGGA  
 GACTTTGGTCTGGCCTGCACAGACATCCTACAGAAGAACACAGACTGGACCAACAGAAAC  
 GGGAAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGCTTACCCGAA  
 CAGTTGGAAGGATCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTGGTCTG  
 CTAGAGCTCTTTCAGCCGTTTGGAAACAGAAATGGAGCGAGCAGAAAGTTCTAACAGGTTA  
 AGAACTGGTCAGTTGCCGGAATCCCTCCGTAAAAGGTGTCCAGTGCAAGCCAAGTATATC  
 CAGCACTTAACGAGAAGGAACTCATCGCAGAGACCATCTGCCATTGAGCTGCTGCAGAGT  
 GAACTTTTCCAAAATCTGGAAATGTTAACCTCACCTACAGATGAAGATAATAGAGCAA  
 GAAAAAGAAATTGCAGAACTAAAGAAGCAGCTAAACCTCCTTTCTCAAGACAAAGGGGTG  
 AGGGATGACGGAAAGGATGGGGGCGTGGGATGA

SEQ ID NO: 74\_17000057519457\_H  
 CACAAGAGCCCTTCTGCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGT  
 AACCACCTACAGGCCGGAAGTGTCCGGGGTGGACGCATTCCGGGTAGCCGAAGAAGTCCCA  
 GGATTGCCGAAGAAGTCCCAGGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTCAG  
 AGACAGCTGATCGGTTGGAGCTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTA  
 CGCCGGCGATGGCGAGGAGCCCGCCCGGAGGCTGAGGCTCTGGCCGAGCCCGGGAGC  
 GGAGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCTGT  
 TCCGTGGCCGCTTCCAGGGCCGCGCGGCGGTGATCAAGCACCGCTTCCCAAGGGCTACC  
 GGCACCCGGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGCAGGAGCCCGGGCGC  
 TCCTCCGCTGTGCGCGCTGGAATATCTGCCCCAGTTGTCTTTTGTGGACTATGCTT  
 CCAACTGCTTATATATGGAAGAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTCAGT  
 CCACTATGGAGACTGAAAAAATCCCCAGGGTCTCTCCAACCTTAGCCAAGACAATTGGGC

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## FIGURE 2III

AGGTTTTGGCTCGAATGCACGATGAAGACCTCATTTCATGGTGATCTCACCACCTCCAACA  
TGCTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTT  
TCATTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCC  
TCAGTACCCATCCCAACACTGAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCAGCT  
CCTCCAAAAAGGCCAGGCCAGTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAA  
AGAGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTT  
TCAAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAG  
ATATTTTAAAGTGGTATGTGATCGTGTCTATTATCATCTGCACTTCACTCAAGAGCTTACT  
ATGTGTCTAAGTCATGTTCTAGGCAGAATTGGGTATTTAAAGTAAATGAGGACAGGCTT  
CTCCCAGATTGTGACATGTATATCTCAGATACATGGGTGTGGCATTGAACCACATAATGA  
GAACATTATTCTCTTTTAGTCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTC  
GCTGAGCTTACTGGCCCTCTAACCAGTGTTTTTTTTTTGTTGTTGTTGTGTACATGTTAT  
ATTTATTTTGAACACAGTTTAAATGGGATACAACCAGCATTTTAAAAAATGAATAGAATA  
CAGCATGGAAAATATCAGTGTATTGTTTTATGAAACTTTACGTGTATATATAGACCAAG  
GATATGTGCTGAGTTTTGATGTCAAATATATTTCTTTTCAGGGTCATGATCAAAAAATG  
AAAAGTCTGCTTAACTCCAATTTCTCTTTTAAAAAAGCAGACTTACAGCTTTCAGGCAAC  
TGAAATTCATGTTAACATGTTTTTATTTTTATTGCTTTGTATTTTTGTGGTTACCTTCTA  
AGACAAGTGATTGATCTAAAGTTCCTTTTAAAGTTTATACCGCTAAACAAACTGAGTTGAT  
TTCTATCACAGGCAGTAAGTAGGTAGAGCAAAAATGGTGAAGTGACTTGTGAAGACTGAA  
GTTTGATGAAGTCTGGTTTAAAGGCACAGGTAAACTGAGTGTGGATGCAAAGTACCAGGA  
GCTAGCTTTTAACTTGCCCAGCCTCAGTTTCTTTTCTTAGAAGAAGCTATGTTTGGGTG  
GGAAGGGAAGAGAGGGATAAGAAAATACCTTTCTTCTGTAACTCCAATCAACAAACA  
TATTTTGAGTGCCTTTTGTGTTCTTGGCACCCCTGTTGGGTATTGGGTACTTGGCACCCCT  
GTTGGGTATTGGGTACAATGGTGAGCCAGACAGACACAGCGCCTGTCCTTTTGTAAAGAT  
ATTTATTTTATAAAAAAGTATAAAGTATACAGTGGGATGTTTTGATATACATTATGAAA  
TGATTGCTACAGCTGAGCTAATTAACACCCATCACCTCACATAGTTACTGTCTTGTCTTCT  
TAATATGGACATTTGCAGCTATGAATTTCCCTCTGCACACTGTTGTCTATCACACACTCTC  
AGTTTTGGTATTTTGTGTTTTTGTTTTTATTTCATCTCAAAGTATTTTCTAATTTCCCTTG  
TGATTTCTTCTTTGACCCCTTGATTGTTTAGAAATCTGTTAATTTCCACACATTTGTAA  
TGTTCCAATTTTCTTTTGTATTGCGAGCTTCATTCCATTGTGTTTCAAGATGATACAG  
TCAGTGCTCTTCTTATGAAGCAAACTTCTATAATAGTAGGACCAGTACCCTGTCTGTT  
TCATTACCAACAGTCAGCATGCCCCAAGTGCCGAGCATGGGGCGGATGGCCAGGAATGAG  
TGAAAACCTTCCCTTCTGCGTAGTTGTGACTAGTAGAGAGGAAAAATAATATAATTGCCT  
GCTTACTGCATGCCAGGCATTGGGCTGGGAATTTTATATTGGATCTAAAATAACTCTTA  
AGTTAGGCATTATCCCCATTTTATAGATGGAGAACTGGCCCCAAAAGGTGGGAACCTGT  
CCAAGACGTCACAGGTAGCAAGAGGTACTTTTACCTGGCTCCAAATCTGTGTTCTTTCCA  
CTGACAAATGAGATATGGGATATGGTGCATCTTTACAGTACTATAATAAGTATTGGCGTA  
TAACATTATTTTCAAGGAACTCCAAGGGCCACAGGAGCTGACAGGTTTTTCAATTAATAT  
TCCCAACATGAATGAGATGCCTCATTCTCAGTTTCTCAGTGTACTATAAGGCTAGTA  
CCTGCTTTGTTGGGGTATGGTTGGCTCGTGTGCATTAAGTCAACAAATCCCTAGT

SEQ ID NO: 75\_AA013524\_M

CTGGTGCAGCAGGGCGCCGAGGCGCGTTCCTGGCCGCTTCCAGGGCCGCGCGGCC  
GTGGTGAAGCACCGCTTCCGAAGAGTTACCGGCACCCGGAGCTGGAGGCGCGGCTCGGC  
CGTCGGCGGACGGTGCAGGAGGCGCGCGCTGCTCCGCTGCCGCCGTGCGGGGATAGCT  
GCCCCAGTCGTCTTCTTTGTGGAATATGCGTCTAACTGCTTATATATGGAAGAAATCGAA  
GACTCGGTGACTGTTTGGGATTATATCCAATCCACTATGGAGACTGAAAAGGACCCCCAG  
TGCCTCTTGGACCTGGCCAGGAGGATGGGGCAGGTTCTGGCCGGAATGCACGACCAAGAC  
CTCATTACGGGGACCTCACCACCTCCAACATGCTCCTGAGGCGGCCCTGGCGCAGCTG  
CACATCGTGCTCATCGACTTTGGGCTGAGCTTTGTCTCAGGACTGCCGGAAGATAAAGGC

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## FIGURE 2JJJ

GTCGACCTCTATGTCTGGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG  
TTTGAAGCCTTTCTGAAGAGTTACGGGGCCTCGTCCAAGAAGTCCAGTCCAGTGTGAAG  
AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTCGGGTAGTGGAGCTGT  
GGTGAACCTGGCTCACGGTGAAGGATGATGTAGACGAGGCTGGACCCCTCAGCAAAGCATG  
GGTTGTTAAGTGGTCTGTGATCGTGTGGGCCACCACCATCCATGGCTCACTGTTCTCAG  
GGGCTTCATGTACATGAGGTTTATTCTGGGCAGAACTGGGTAGGTAGCCCAGGCTAGCCT  
TGAATTTATGGCAACATCCTACCTCAGCTTGCTTGAAGAGGTTATAAGCCACCATACT  
GACTTTGCACTGATTCTGTGAGAAAC

SEQ ID NO: 76\_17000139801197\_H, IRAKM\_H  
ATGGCGGGGAACGTGTGGGGCCGCGCGCGCTGTGCGGCACACGCTGCTGTTGACCTG  
CCGCCGCGCTGCTCGGAGAGCTCTGCGCTGTTCTGGACAGCTGCGACGGCGCGCTGGGC  
TGGCGCGGCTGGCAGAGAGACTTTCAAGCAGCTGGCTGGATGTTTCGTTCATATTGAAAAG  
TATGTAGACCAAGGTAAAAGTGAACAAGAGAATTACTTTGGTCCTGGGCACAGAAAAAC  
AAGACCATCGGTGACCTTTTACAGGTCTCCAGGAGATGGGACATCGTCGAGCTATTCAT  
TTAATTACAACTATGGAGCAGTGTGAGTCTTCAGAGAAGAGTTATCAGGAAGGTGGA  
TTTCCAAATATATTATTCAAGGAAACAGCCAATGTCACCGTGGATAATGTTCTTATTCCT  
GAACATAATGAAAAAGGAGTACTGCTTAAATCTCCATCAGCTTTCAAATATCATAGAA  
GGAAGTAGAAATTTCCACAAAGACTTCCTAATTGGAGAAGGAGAGATTTTGGAGGTATAC  
AGAGTGGAGATTCAAACCTAACATATGCTGTCAAATTATTTAAACAGGAGAAAAAATG  
CAGTGTAAGAAGCATTGGAAGAGGTTTTTATCTGAGCTTGAAGTTTACTACTGTTTCAT  
CACCCAAACATACTAGAGTTGGCTGCATATTTTACAGAGACTGAGAAGTTCTGTCTGATT  
TATCCATACATGAGAAATGGAACACTTTTTGACAGATTGCAGTGTGTAGGTGACACGGCC  
CCACTCCCTTGGCACATTGCAATCGGTATATTAATAGGAATATCCAAAGCCATTCACTAC  
CTGCACAACGTTCAACCATGCTCGGTTCATCTGTGGCAGTATATCAAGTGCAAAACATCCTT  
TTGGATGATCAGTTTCAACCCAACTAACTGATTTTGCCATGGCACACTTCCGGTCCCAC  
CTAGAACATCAGAGTTGTACCATAAATATGACCAGCAGCAGCAGTAAACATCTGTGGTAC  
ATGCCAGAAGAGTACATCAGACAGGGGAACTTTCCATTAAACAGATGTCTACAGCTTT  
GGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTGTAGATGATCCAAACAT  
ATCCAGCTGCGGGATCTCCTTAGAGAAATGATGGAGAAGAGAGGCTGGATTTCATGTCTC  
TCATTTCTAGATAAGAAAGTGCCTCCCTGCCCTCGGAATTTCTCTGCCAAGCTCTTCTGT  
TTGGCAGGCCGGTGTGCTGCAACGCGGGCAAAGTTAAGACCATCAATGGATGAAGTTTTA  
AATACTCTTGAAAGTACTCAAGCCAGCTTGTATTTTGTGCTGAAGATCCTCCCACATCACTA  
AAGTCTTCAGGTGTCCTTCTCCTCTATTCTTGGAAGATGTACCAAGTATTCCAGTGGAA  
GATGATGAAAGCCAGAATAACAATTTACTACCTTCTGATGAAGGCCTGAGGATAGACAGA  
ATGACTCAGAAAACTCCTTTTGAATGCAGCCAGTCTGAGGTTATGTTTCTGAGCTTGGAC  
AAAAAGCCAGAGAGCAAGAGAAATGAGGAAGCTTGCAACATGCCAGTTCCTCTTGTGAA  
GAAAGTTGGTTCCCAAAGTATATAGTTCCATCCCAGGACTTAAGGCCCTATAAGGTAAAT  
ATAGATCCTTCTTCAGAAGCTCCAGGGCATTCTTGCAAGGAGCAGGCCAGTGGAGAGCAGC  
TGTTCTCCAAATTTTCTGGGATGAATATGAACAGTACAAAAAAGAATAA

SEQ ID NO: 77\_AA840598\_M IRAKM\_M  
ATGTGGAAGAGATTTTATCAGAACTGGAAGTTCTACTCCTGTTCCGTCACCCCCACATA  
CTAGAGCTGGCTGCATATTTACGGAGACTGAGAACTTTGTCTGGTTTATCCCTATATG  
AGCAACGGGACGCTTTTCGACAGATTACAGTGCACAAATGGCACAACCCCGCTTTCTGG  
CACGTTGCAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGACAACACT  
CAGCCGTGCGCCGTATCTGTGGCAACGTTTCCAGTGCAAACTACTCTGGATGACCAG  
CTCCAACCCAACTAACGGATTTTGTGCTGAGCGCACTTCCGACCCAATCTAGAGCAGCAG  
AGTTCTACCATAAATATGACCGGCGGTGGCAGGAAACATCTGTGGTACATGCCAGAAGAA

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FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAAACTGATGTCTACAGCTTCGGAATCGTGATC  
 ATGGAGGTTCTAACGGGCTGCAAAGTGGTGTCTGGATGACCCGAAACACGTTTCAGCTGCGG  
 GACCTCCTCATGGAAGTGTGGAGAAAAGAGGCCTAGACTCCTGCCTGTCCTTCTTAGAC  
 AGGAAGATACCACCCTGTCCTCGGAACCTTCTCTGCAAAGCTCTTCTCTCTGGCGGGCCGG  
 TGTGTGGCAACGAAGGCCAAGTTAAGACCCACGATGGACGAAGTCCCTGTCCTCTCTGGAG  
 AGCACCAGCCTAGCTTGTATTTTGCAGAAGACCCTCCCACGTCCTTGAAGTCCCTCAGG  
 TGTCTTCTCCACTGTTCTTGGATAATGTCCCAAGTATTCCAGTAGAAGATGATGAAAAC  
 CAGAATAACCATTTCAGTACCTCCCAAGGAAGTTTGGGGACAGATAGAGTGAAGTACAGAAA  
 ACCCCCTTTGAATGCAGCCAGTCTGAGGTCACCTTTCTAGGCTTGGACCGAAACAGAGGG  
 AACAGGGGAAGTGAAGCGGATTGCAACGTGCCCAGTTCTTCTCATGAGGAATGCTGGTCC  
 CCAGAGCTTGTGGCGCCATCCCAGGACTTAAGTCCCTACTGTGATCAGTTTGGGCTCGTCT  
 TGGGAAGTACCAGGCCATTCTTATGGGAGCAAGCCAATGGAGAAGAGGTGTTCTCTGGG  
 CTCTTTTGCAGTGAGCATGAACAGTCCAAAAGCAGTGAATCCACCAGAAGATCAAGCAA  
 AAAATAAAAGCAAACGTCACTGAAGGCATGAGCAAAATAGCATCCCCGTGAAAAGACACG  
 AGCTCTGAGCTCCGTGAGTACAGCCAAGGGACCAACTGATGGAGAATTTGAATGGTGCAG  
 ATTAGCAGCAAGGAAGTCTATTCTTCTCCAAACAGAATAATTTCAAGAGATGCTTTAT  
 TCAAGTGACCGCTCTCAGTCAAACCTGAGAAGCTAAACTGGAGCCAATCAGAATTATCC  
 AAGATTCCGGGTCTTGACAACCAAAACCTAGCAAAGAGTAGCAGGACAAGTCTCTCTCTT  
 AAGTCTCTCACTCTCTCTCATCATCCGAGTGAGATCTTGGTATAGGTGAACAGAGAACCA  
 CCCACCTTCCAGAACCAGAACCACCTTCTCCCCAAGCCAGCAGTCACTCACTCACCATCA  
 GCAGCCAGTAGTCACCAGCAGCCAATCATGATACAGTGTCACTCTCCCTCTGCGCATGCC  
 CTACGTCTTTTATAAAACCAGGTCTTCAGGGCCCCACCCCTTTCTTTTCCATCCTTGCT  
 CAGAGGCAGCCTTTTGTATACATTCCCTGACCCCAACCCCAATTATATCTCTCATATGATA  
 TCTGTTGCGTAGTGTGACTTTGTGGCATGACTTGGTTGTCAGATCATTTGCACAAGAACA  
 AGCGAATACACAACAACAAAGCCCACCATCATTACCACCGGCACTTAATGCTAGTCTTTC  
 TGCTAGGGATACTGACAGTCTATTTGCTTCCCATGGTTCATAGGGAAGTTGCTCAAATGCA  
 AAGGTTGTAGGGAATGTCTAATTTGTAAATGGCGTCGGGTGCCTTTGGAAGGAATTGTGT  
 TTTTACAGCCAGTTGCTACTCTTGTATTATCGCTGGTTAACCAGTCTGTCCGGAAGTGAGC  
 CAAGTCATCCTTGCTAGGGCTTTTTCTGTGTAGAGAGGGAATTCAGTCCAAAGTCTGCT  
 TCTCTGTATTTAAATTCTTAGAAGAGTTGCCTGTGGCATTCCAATTGTTATATAAAAAA  
 TTATATTAAAGAATTCCAGCACT

SEQ ID NO: 78\_AA088547\_H

ATGGCGAGTGCAGGTCAGGGGGTTCGAGGCCGTGGCCCCGGCTGGGGCTCCAGCTCCAGTTC  
 GCGGCGCTGCTGCTCGGGACGCTGAGTCCACAGGTTCTACTCTCAGGCCAGAGAACCTC  
 CTGCTGGTGTCCACCTTGGATGGAAGTCTCCACGCACTAAGCAAGCAGACAGGGGACCTG  
 AAGTGGACTCTGAGGGATGATCCCGTCATCGAAGGACCAATGTACGTACAGAAATGGCC  
 TTTCTCTCTGACCCAGCAGATGGCAGCCTGTACATCTTGGGGACCCAAAAACAACAGGGA  
 TTAATGAAACTGCCATTCAACATCCCTGAGCTGGTTCATGCCTCTCCCTGCCGCAGCTCT  
 GATGGGGTCTTCTACACAGGCCGGAAGCAGGATGCCTGGTTTGTGGTGGACCCTGAGTCA  
 GGGGAGACCCAGATGACACTGACCACAGAGGGTCCCTCCACCCCCCGCCTCTACATTGGC  
 CGAACACAGTATACGGTCACCATGCATGACCCAAGAGCCCCAGCCCTGCGCTGGAACACC  
 ACCTACCGCCGCTACTCAGCGCCCCCATGGATGGCTCACCTGGGAAATACATGAGCCAC  
 CTGGCGTCTGCGGGATGGGCCTGCTGCTCACTGTGGACCCAGGAAGCGGGACGGTGTCTG  
 TGGACACAGGACCTGGGCGTGCCTGTGATGGGCGTCTACACCTGGCACCAGGACGGCCTG  
 CGCCAGCTGCCGCATCTCACGCTGGCTCGAGACACTCTGCATTTCTCGCCCTCCGCTGG  
 GGCCACATCCGACTGCCTGCCTCAGGCCCCCGGGACACAGCCACCCTCTTCTCTACCTTG  
 GACACCCAGCTGCTAATGACGCTGTATGTGGGGAAGGATGAACTGGCTTCTATGTCTCT  
 AAAGCACTGGTCCACACAGGAGTGGCCCTGGTGCCTCGTGGACTGACCCTGGCCCCCGCA  
 GATGGCCCCACCACAGATGAGGTGACACTCCAAGTCTCAGGAGAGCGAGAGGGCTCACCC

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## FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCATT  
GGACACCAAGAGCTACCCCCAGTCTGCACACCACCATGCTGAGGGTCCATCCCACCTTG  
GGGAGTGGAACTGCAGAGACAAGACCTCCAGAGAATACCCAGGCCCCAGCCTTCTTCTTG  
GAGCTATTGAGCTTGAGCCGAGAGAACTTTGGGACTCCGAGCTGCATCCAGAAGAAAAA  
ACTCCAGACTCTTACTTGGGGCTGGGACCCCAAGACCTGCTGGCAGCTAGCCTCACTGCT  
GTCCTCCTGGGAGGGTGGATTCTCTTTGTGATGAGGCAGGTGGTGGAGAAGCAGCAGGAG  
ACCCCTTGGCACCTGCAGACTTTGCTCACATCTCCAGGATGCCCCAGTCCCTGCACTCG  
GGGGCCAGCCGGAGGAGCCAGAAGAGGCTTCAGAGTCCCTCAAAGCAAGCCCAGCCACTC  
GACGACCCTGAAGCTGAGCAACTCACCGTAGTGGGGAAGATTTCCCTTCAATCCCAAGGAC  
GTGCTGGGCCCGGGGGCAGGCGGGACTTTCGTTTTCCGGGGACAGTTTGAGGGACGGGCA  
GTGGCTGTCAAGCGGCTCCTCCGCGAGTGCTTTGGCCTGGTTCGGCGGGAAGTTCAACTG  
CTGCAGGAGTCTGACAGGCACCCCAACGTGCTCCGCTACTTCTGCACCGAGCGGGGACCC  
CAGTTCCACTACATTGCCCTGGAGCTCTGCCGGGCTCCTTGCAGGAGTACGTAGAAAAC  
CCGGACCTGGATCGCGGGGGTCTGGAGCCCGAGGTGCTGCTGCAGCAGCTGATGTCTGGC  
CTGGCCACCTGCACTCTTTACACATAGTGCACCGGGACCTGAAGCCAGGAAATATTCTC  
ATCACCGGGCCTGACAGCCAGGGCCTGGGCAGAGTGGTGTCTCTCAGACTTCGGCCTCTGC  
AAGAAGCTGCCTGCTGGCCGCTGTAGCTTCAGCCTCCACTCCGGCATCCCCGGCACGGAA  
GGCTGGATGGCGCCCGAGCTTCTGCAGCTCCTGCCACCAGACAGTCTTACCAGCGCTGTG  
GACATCTTCTCTGCAGGCTGCGTGTCTACTACGTGCTTTCTGGTGGCAGCCACCCCTTT  
GGAGACAGTCTTTATCGCCAGGCAAACTCCTCACAGGGGCTCCCTGTCTGGCTCACCTG  
GAGGAAGAGGTCCACGACAAGGTGGTTGCCGGGACCTGGTTGGAGCCATGTTGAGCCCA  
CTGCCGAGCCACGCCCCCTCTGCCCCCCAGGTGCTGGCCACCCCTTCTTTTGGAGCAGA  
GCCAAGCAACTCCAGTTCTTCCAGGACGTGAGTACTGGCTGGAGAAGGAGTCCGAGCAG  
GAGCCCCTGGTGAGGGCACTGGAGGCGGGAGGCTGCGCAGTGGTCCGGGACAACTGGCAC  
GAGCACATCTCCATGCCGCTGCAGACAGATCTGAGAAAGTTCCGGTCTTATAAGGGGACA  
TCAGTGCAGAGACCTGCTCCGTGCTGTGAGGAACAAGAAGCACCCTACAGGGAGCTCCCA  
GTTGAGGTGCGACAGGCACTCGGCCAAGTCCCTGATGGCTTCGTCCAGTACTTCACAAAC  
CGCTTCCACGGCTGCTCCTCCACACGCACCGAGCCATGAGGAGCTGCGCCTCTGAGAGC  
CTCTTCCCTGCCCTACTACCCGCCAGACTCAGAGGCCAGGAGGCCATGCCCTGGGGCCACA  
GGGAGGTGA

SEQ ID NO: 79\_HGP\_6644466

GGAGGGTTGCAATTGCAACGGCAGCTGCCGGCGTATGTGTTGGTGTCTAGAGGCAGCTGC  
AGGGTCTCGCTGGGGGCGCTCGGGACCAATTTTGAAGAGGTACTTGGCCACGACTTATT  
TTCACCTCCGACCTTTCCTTCCAGGCGGTGAGACTCTGGACTGAGAGTGGCTTTCACAA  
GGAAGGGATCAGTAATTTCAAGACACCAAGCAATTATCAGAAAAAAGAAATCTGTATT  
ATGTTCAACTCCAATAATAATATCCCGGCTCTCCGTTTATGCAGAAGCTTGGCTTTGG  
TACTGGGGTAAATGTGTACCTAATGAAAAGATCTCCAAGAGGTTTGTCTCATTCTCCTTG  
GGCTGTAAAAAAGATTAATCCTATATGTAATGATCATTATCGAAGTGTGTATCAAAAGAG  
ACTAATGGATGAAGCTAAGATTTTGAAGAGCCTTCATCATCCAAACATTGTTGGTTATCG  
TGCTTTTACTGAAGCCAATGATGGCAGTCTGTGTCTTGCTATGGAATATGGAGGTGAAAA  
GTCTCTAAATGACTTAATAGAAGAACGATATAAAGCCAGCCAAGATCCTTTTCCAGCAGC  
CATAATTTTAAAGTTGCTTTGAATATGGCAAGAGGGTTAAAGTATCTGCACCAAGAAAA  
GAACTGCTTCATGGAGACATAAAGTCTTCAAATGTTGTAATTAAGGCGATTTTGAAC  
AATTAATACTGTGATGTAGGAGTCTCTTACCCTGGATGAAAAATATGACTGTGACTGA  
CCCTGAGGCTTGTTACATTGGCACAGAGCCATGGAAACCCCAAGAGCTGTGGAGGAGAA  
TGGTGTATTACTGACAAGGCAGACATATTTGCCCTTTGGCCTTACTTTGTGGGAAATGAT  
GACTTTATCGATTCCACACATTAATCTTTCAAATGATGATGATGATGAAGATAAACTTT  
TGATGAAAGTGATTTTGATGATGAAGCATACTATGCAGCGTTGGGAACTAGGCCACCTAT  
TAATATGGAAGAACTGGATGAATCATAACGAAAGTAATTGAACTCTTCTGTATGCAC

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## FIGURE 2MMM

TAATGAAGACCCCTAAAGATCGTCCTTCTGCTGCACACATTGTTGAAGCTCTGGAAACAGA  
TGTCTAGTGATCATCTCAGCTGAAGTGTGGCTTGGCGTAAATAACTGTTTATTCCAAAATA  
TTTACATAGTTACTATCAGTAGTTATTAGACTCTAAAATTGGCATATTTGAGGACCATAG  
TTTCTTGTTAACATATGGATAACTATTTCTAATATGAAATATGCTTATATTGGCTATAAG  
CACTTGGAAATTGTACTGGGTTTTCTGTAAAGTTTTAGAACTAGCTACATAAGTACTTTG  
ATACTGCTCATGCTGACTTAAAACACTAGCAGTAAAACGCTGTAACTGTAAACATTAAAT  
TGAATGACCATTACTTTTATTAATGATCTTTCTTAAATATTCTATATTTTAATGGATCTA  
CTGACATTAGCACTTTGTACAGTACAAAATAAAGTCTACATTTGTTTAAAACACTGAACC  
TTTTGCTGATGTGTTTATCAAATGATAACTGGAAGCTGAGGAGAATATGCCTCAAAAAGA  
GTAGCTCCTTGGATACTTCAGACTCTGGTTACAGATTGTCTTGATCTCTTGGATCTCCTC  
AGATCTTTGGTTTTTGGCTTTAATTTATTAAATGTATTTTCCATACTGAGTTTAAAATTTA  
TTAATTTGTACCTTAAGCATTTCAGCTGTGTAAAAACAATAAACTCAAATAGGATGA  
TAAAGAATAAAGGACACTTTGGGTACCAGAAGGTGTCTCAGCATTATTTTATACTTC

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ATCTCCAAGAGGGTTGTCTCATTCTCCTTGGGCGGTGAAAAAGATAAGTCTTTTATGCGA  
TGATCATTATCGAACTGTGTATCAGAAGAGACTAACTGATGAAGCTAAGATTTTAAAAAA  
CCTTAATCACCCAAACATTATAGGATATCGTGCTTTTACTGAAGCCAGTGATGGTAGTCT  
GTGCCTTGCTATGGAGTATGGAGGTGAAAAGTCTCTGAATGACTTAATAGAAGAGCGGAA  
CAAAGACAGTGGAAAGTCCTTTTCCAGCAGCTGTAATTCTCAGAGTTGCTTTGCACATGGC  
CAGAGGGCTAAAGTACCTGCACCAAGAAAAGAAGCTGCTTCATGGAGACATAAAGTCTTC  
AAATGTTGTAATTAAAGGTGATTTTGAACAATTAAAATCTGTGATGTAGGAGTCTCTCT  
GCCATTGGATGAAAATATGACTGTGACTGATCCTGAGGCCTGTTATATTGGTACTGAGCC  
ATGGAAACCCAAGGAAGCGTTGGAAGAAAATGGCATCATTACTGACAAGGCAGATGTGTT  
TGCTTTTGGCCTTACTCTGTGGGAAATGATGACTTTATGTATTCCACACGTCATCTTCC  
AGATGATGATGTTGATGAAGATGCAACCTTTGATGAGAGTGACTTCGATGATGAAGCATA  
TTATGCAGCTCTGGGGACAAGGCCATCCATCAACATGGAAGAGCTGGATGACTCCTACCA  
GAAGGCCATTGAACTCTTCTGTGTGTGCACTAATGAGGATCCTAAAGATCGCCCGTCTGC  
TGCACACATCGTTGAAGCTTTGGAAGTAGATGGCCAATGTTGTGGTCTAAGCTCAAAGCA  
TTAACTTGATGGAAGTGTAACTAGATATATGTAGTTAATATAACTTATGGTAGCTAG  
ATTCTAGAAGTAGCTTTAACACTAGTGACCCCTGTCTAAGATGACTTAAGAATCAAGGGA  
CCATTGCTTTGTACAGATCTTTTATGATATTCTTGCTTCTTTAGTGGGTACTAAAAAT  
TTCCTACGTACATGTGGTACAGATATCTGTCTGCTCATAGTGTGAGTCTTCAGCTGGC  
CTGTCAGCCCATGCGCCCTGGGACTTGAGAAGAGTTTATAAACGTAGCTCCTAGGGTGTG  
TTGCCTCTCTACACTTAGCTTCTAATTTATTACTTTGTTTCTACTGATTGTGTCTTAAGT  
CTTTTAAATAAATGTAAGAATAAACAATAAAAGACAGTTTTTAGTACCAGG

SEQ ID NO: 81\_5R57\_10\_2\_M TESK2\_M

GCTGCTGGACAGTGACTTGTATTTACCGTGGACTGTGAGAGTGAAACTGGCCTATGGCAT  
AGCAGTGGGCCTCAGCTACCTTCACTTCAAAGGCATTTTCCATCGGGACCTCACATCAA  
GGTGTGAAGGCTTTGCTTTC

SEQ ID NO: 82\_AA232253\_H

ATGTCGTCTCTCGGTGCCTCCTTTGTGCAAATTAAATTTGATGACTTGACGTTTTTTGAA  
AACTGCGGTGGAGGAAGTTTGGGAGTGTTTATCGAGCCAAATGGATATCACAGGACAAG  
GAGGTGGCTGTAAAGAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTTC  
AGTCACAGAAACATCATCCAGTTTTATGGAGTAATCTTGAACCTCCCACTATGGCATT  
GTCACAGAATATGCTTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAG  
GAGATGGATATGGATCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTAT  
TTACATATGGAGGCTCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTT

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## FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCAT  
ACAACACACATGTCCTTGGTTGGAACCTTTCCCATGGATGGCTCCAGAAGTTATCCAGAGT  
CTCCCTGTGTCAGAACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTA  
ACAAGGGAGGTCCCCCTTTAAAGGTTTGGAAAGGATTACAAGTAGCTTGGCTTGTAGTGAA  
AAAAACGAGAGATTAACCATTTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAACTGTTACAT  
CAGTGTGGGAAGCTGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCATCCTG  
GAGTCCATGTCAAATGACACGAGCCTTCCTGACAAGTGTAACCTATTCTACACAACAAG  
GCGGAGTGGAGGTGCGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGAT  
CTCAGCTTTAAGGAGCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAA  
AAGCTGACAGAGCAGTCCAACACCCCGCTGCTGCCTTCTTTGAGATTGGTGCATGGACG  
GAAGACGATGTGTATTGGTGGGTTCAGCAGCTCGTCAGAAAAGGTGACTCTTCAGCAGAG  
ATGAGTGTATATGCAAGCTTGTTTAAAGAAAACAACATTACAGGGAAGCGGCTGCTGCTG  
CTGGAGGAAGAAGACCTGAAAGACATGGGCATTGTCTCCAAGGGGCATATCATTCACTTC  
AAGTCAGCCATTGAGAAATTAACCCATGATTACATAAAATTTGTTTCACTTCCCACCACTA  
ATTAAGGACTCAGGAGGTGAACCTGAAGAAAATGAGGAAAAAATAGTGAACCTGGAAGTG  
GTTTTTGGTTTTCACTTGAAACCAGGAAGTGGCCACAGGATTGTAAGTGGAAGATGTAT  
ATGGAGATGGATGGGGATGAAATTGCAATAACCTACATAAAAGATGTGACATTCAACACT  
AACCTACCTGATGCGGAGATTTTAAAGATGACAAAGCCACCATTGTAAATGGAGAAGTGG  
ATTGTAGGAATAGCAAAAAGTCAGACTGTGGAGTGCACGTGTCACATATGAGAGTGATGTT  
AGAAGTCCAAAAAGCACTAAACATGTCCATTGATTGAGTGGAGTAGAACAACCTCAG  
GATGAAGTGAAAGCAGTCCAACCTTGCCATTGAGACATTATTCACCAATTCAGATGGCAAC  
CCTGGAAGCAGGTCCGACTCAAGTGCTGATTGCCAGTGGTTAGATACTCTGAGGATGCGG  
CAGATTGCATCCAACACTTCTTTACAGCGTTCCCAGAGCAATCCTATTCTGGGGTCAACCG  
TTCTTCTCACACTTTGATGGCCAGGATTCTACGCTGCTGCTGTGAGACGGCCCCAGGTG  
CCCATTAAAGTATCAACAGATTACACCTGTGAACCAGTCCAGAAGCTCGTCTCCTACTCAG  
TATGGACTGACCAAAAACCTTCTCTTCTTACATCTCAACTCTAGGGACAGTGGCTTTTCC  
AGTGGCAATACTGACACCTCTTCAGAGAGGGGTGATACTCAGACAGAAGCAGGAACAAA  
TATGGACGTGGTAGTATATCACTCAATTCTTCTCTAGAGGAAGATACAGTGGAAAGAGT  
CAGCATTCCATCCATCAAGAGGAAGATACCCTGGAAAGTTCTACAGGGTTTCTCAGTCA  
GCACTCAATCCTCACCAGTCGCCTGACTTCAAGAGAAGCCCCAGGGACCTCCACCAACCC  
AACACCATAACCAGGGATGCCTTTGCACCCTGAGACTGACTCAAGAGCCAGTGAAGAGGAC  
AGCAAAGTCAGCGAAGGGGGCTGGACAAAAGTGAATAACCGGAAAAAGCCCCACAGGCCA  
TCTCCCGCCAAAACCAATAAAGAGAGAGCCAGAGGGGACCACCGTGGATGGAGAACTTT  
TGA

SEQ ID NO: 83\_AI375137\_H  
ATGGGAAATTATAAATCTAGACCAACCCAACTTGTAAGTGAATGGAAGAAAAAAGTC  
AGTGAATCATATGTTATCACAATAGAAAGATTAGAAGATGACCTGCAGATCAAGGAAAAA  
GAACTGACAGAACTAAGGAATATATTTGGCTCTGATGAAGCCTTCAGTAAAGTCAATTTA  
AATTACCGCACTGAAAATGGGCTGTCTCTACTTCATTATGTTGCATTTGTGGAGGCAAG  
AAATCACATATTCGAACTCTTATGTTGAAAGGGCTCCGCCCATCTCGACTGACAAGAAAT  
GGATTTACAGCCTTGCAATTTAGCAGTTTACAAGGATAATGCAGAATTGATCACTTCTCTG  
CTTCACAGTGGAGCTGATATACAGCAGGTGGATACGGTGGCCTCACTGCCCTCCATATT  
GCTACAATAGCTGGCCACCTAGAGGCTGCTGATGTGCTGTTGCAACATGGAGCTAATGTC  
AATATTCAAGATGCAGTTTTTTTTCACTCCATTGCATATTGCAGCGTACTATGGACATGAA  
CAGGTAAGTGCCTTCTTTTGAATTTGGTGTGATGTAATGTAAGTGGTGAAGTTGGA  
GATAGACCCCTCCACCTAGCATCTGCAAAAGGATTCTTGAATATTGCAAACTCTTGATG  
GAAGAAGGCAGCAAAGCAGATGTGAATGCTCAAGATAATGAAGACCATGTCCCCTCCAT  
TTCTGTTCTCGATTTGGACACCATGATATAGTTAAGTATCTGCTGCAAGTGAATTTGGA  
GTTCAACCTCATGTTGTTAATATCTATGGAGATACCCCTTACACCTGGCATGCTACAAAT

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FIGURE 2000

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG  
GAAAACATCTTCAGTGAAACAGCTTTTTCATAGTGCTTGTACCTATGGCAAGAGCATTGAC  
CTAGTCAAATTTCTTCTTGATCAGAATGTCATAAACATCAACCACCAAGGAAGGGATGGG  
CACACTGGATTACACTCTGCTTGCTACCACGGTCACATTCGCCTGGTTCAGTTCTTACTG  
GATAATGGAGCTGATATGAATCTAGTGGCTTGTGATCCCAGCAGGTCTAGTGGTGAAAAA  
GATGAGCAGACATGTTTGATGTGGGCTTATGAAAAAGGGCATGATGCCATTGTACACTC  
CTGAAGCATTATAAGAGACCACAAGATGAATTGCCCTGTAATGAATATTCTCAGCCTGGA  
GGAGATGGCTCCTATGTGTCTGTTCCATCACCTTGCGGAAGATTAAAAGCATGACAAAA  
GAGAAGGCAGATATTCTCCTCCTAAGAGCTGGATTGCCTTCACATTCCATCTTCAGCTC  
TCAGAAATTGAGTTCATGAGATTATTGGCTCAGGTTCTTTTGGGAAAGTATATAAAGGA  
CGATGCAGAAATAAAATAGTGGCTATAAAACGTTATCGAGCCAATACCTACTGCTCCAAG  
TCAGATGTGGATATGTTTGGCCGAGAGGTGTCCATTCTCTGCCAGCTCAATCATCCCTGC  
GTAATTGAGTTTGTGGGTGCTTGCTTGAATGATCCCAGCCAGTTTGCCATTGTCACTCAA  
TACATATCAGGGGGTCTCTGTTCTCCCTCCTTCATGAGCAGAAGAGGATTCTTGATTG  
CAGTCTAAATTAATTATTGCAGTAGATGTTGCCAAAGGCATGGAGTACCTTCACAACCTG  
ACACAGCCAATTATACATCGTGAAGTGAACAGTCACAATATTCTTCTCTATGAGGATGGG  
CATGCTGTGGTGGCAGATTTTGGAGAAATCAAGATTTCTACAGTCTCTGGATGAAGACAAC  
ATGACAAAAACAACCTGGGAACCTCCGTTGGATGGCTCCTGAGGTGTTACGCAGTGCCT  
CGGTACACCATCAAAGCAGATGTCTTCAGCTATGCTCTGTGTCTGTGGGAAATTCTCACT  
GGCGAAATTCCATTGCTCATCTCAAGCCAGCGGCTGCGGCAGCAGACATGGCTTACCAC  
CACATCAGACCTCCCATTTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGA  
GGGTGGAACGCATGTCTGAAGGAAGACCCGAATTTTCTGAAGTTGTGATGAAGTTAGAA  
GAGTGTCTCTGCAACATTGAGCTGATGTCTCTGCTCAAGTAACAGCAGTGGGTCTCTC  
TCACCTTCTTCTTCTTCTGATTGCCTGGTGAACCGGGGAGGACCTGGCCGGAGTCATGTG  
GCAGCATTAAAGAAGTCGTTTCGAATTGGAATATGCTCTAAATGCAAGGTCCTATGCTGCT  
TTGTCCCAAAGTGCTGGACAATATTCCTCTCAAGGTCTGTCTTTGGAGGAGATGAAAAGA  
AGTCTTCAATACACACCCATTGACAAATATGGCTATGTATCCGATCCCATGAGCTCAATG  
CATTTTCATTCTTGCCGAAATAGTAGCAGCTTTGAGGACAGCAGCTGA

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ATGATTTCTTGCTGTNATAACCTATGCACTCACAAAGATGAACTCTCTGAGAGGGATGA  
GCAAGAGCTTCAGGAAATCCGAAAGTATTTCTCCTTTCCTGTATTCTTTTTCAAAGTGCC  
GAAACTGGGCTCGGAGATAATAGACTCCTCAACCAGGAGAATGGAGAGCGAAAGATCACC  
GCTTTATCGCCAGCTAATTGACCTGGGCTATCTGAGCAGCAGTCACTGGAAGTGTGGGGC  
TCCTGGCCAGGATACTAAAGCTCAGAGCATGTTGGTGGAAACAGAGTGAAAAGCTGAGACA  
CTTGAGCACATTTTCTCACCAGGTGTTACAGACTCGCCTGGTGGATGCAGCCAAGGCCCT  
GAACCTGGTGCCTGCACTGCCCTTGACATCTTTATTAACCAGGCATTTGACATGCAGCG  
GGACCTGCAGATCACTCCCAAACGTCTGGAATATACTCGAAAAAGGAGAATGAGTTGTA  
TGAATCATTGATGAATATTGCCAACCGAAAGCAGGAGGAAATGAAGGATATGATTGTTGA  
GACACTTAATACCATGAAGGAGGAACCTTCTGGATGATGCTACTAACATGGAGTTTAAAGA  
CGTCATTGTCCCTGAGAATGGAGAACCAGTAGGCACCAGAGAGATCAAATGCTGCATCCG  
ACAGATCCAGGAACTCATCATCTCCCGACTTAATCAGGCAGTGGCTAATAAGCTGATCAG  
CTCAGTGGATTACCTGAGGGAAAGCTTCGTGCGAACCCCTGGAACGATGTCTGCAGAGCCT  
GGAGAAGTCTCAGGATGTCTCAGTTCACATCACCAGTAATTATCTCAAACAGATCTTAAA  
TGCTGCCTATCATGTTGAAGTCACGTTTCACTCAGGGTCGTGAGTTACAAGGATGCTATG  
GGAGCAAATCAAACAGATCATCCAGCGCATCACATGGGTGAGCCACCTGCCATCACTCT  
GGAATGGAAGAGGAAGGTGGCCAGGAAGCCATTGAGAGCCTCAGCGCCTCCAAATTGGC  
TAAGAGCATTTGCAGCCAATTCCGGAAGCTCGGCTCAATAGTTCCACAGAGGCTTTTGCAGC  
CTCCTTGCGGCAGCTGGAAGCTGGCCACTCAGGCCGCTTAGAGAAAAAGGAAGATCTATG  
GCTGAGGGTTCGGAAAGATCATGCTCCCCGCCTGGCCCCGCTTTCTCTGGAAGCCGTT



## FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCCA  
GTATGGTGTGGTATACCTGTGTGACAACTGGGGAGGACACTTCCCTTGTGCCCTCAAATC  
AGTTGTCCCTCCAGATGAGAAGCACTGGAATGATCTGGCTTTGGAATTTCACTATATGAG  
GTCTCTGCCGAAGCATGAGCGATTGGTGGATCTCCATGGTTTCACTATTGACTACAACCTA  
TGGTGGTGGCTCCAGCATTGCTGTGCTCCTCATTATGGAGCGGCTACACCGGGATCTCTA  
CACAGGGCTGAAGGCTGGGCTGACCCTGGAGACACGTTTGCAGATAGCACTAGATGTGGT  
GGAGGGAATCCGCTTCTGACAGCCAGGCACTTGTCCATCGTGATATCAAACCTGAAAAA  
TGTGCTGCTGGATAAGCAGAACCGTGCCAAGATCACTGACTTAGGATTCTGCAAGCCAGA  
GGCCATGATGTCAGGCAGCATTGTGGGGACACCAATCCATATGGCCCCTGAACTTTTCAC  
AGGGAAGTACGATAATTCCGTGGATGTCTACGCTTTTGGAAATTCCTTTCTGGTATATCTG  
CTCAGGCTCTGTCAAGCTCCCTGAGGCATTTGAGAGGTGTGCTAGCAAAGACCATCTCTG  
GAACAATGTGCGGAGGGGGGCTCGCCCAGAAGCTCTTCTGTGTTTGATGAGGAGTGCTG  
GCAGTTGATGGAAGCCTGTTGGGATGGCGACCCCTTGAAGAGGCCTCTCTTGGGCATTGT  
CCAGCCCATGCTCCAGGGCATCATGAATCGGCTCTGCAAGTCCAATTCTGAGCAGCCAAA  
CAGAGGACTAGATGATTCTACTTGAAAGCAAAGACCTTTCTCTTTCACTCTCTAGTTATT  
TCCTTCCCCCTCACCATTGCGCCATGGGGAGAATTTGACATTTATTCACTATAGGACACA  
CTCCCAAGGGAACCTGGTGCTTGTGCTGGGAACTTGAACCTTCCAGGCAGGGATGACTCC  
TGGACAGTGAAGAGTTGAATGACTGAGCATATTGAGCAGCTCACTGAAGCGCCAAGCTAT  
CCCTTTAGCAAAAAGTGTCTCAGATGTGTAAAAGCTGAGGAATGTGGTGTCTTGGCTTC  
ACAAATGAAAAGGAGGCAGATGTT

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TTGATGTCAACCTGAAGGCTTCTAAAGCGAGTGATGTCTACAGCTTTGGGATCCTCGTGT  
GGGCAGTGCTGGCTGGCAGAGAAGCTGAGTTGGTAGACAAGACTTCACTAATCCGGGAAA  
CAGTGTGTGACAGGCAGAGTCGTCCTCCACTGACAGAGCTGCCTCCAGGTAGCCCTGAGA  
CTCCCGGCTTGGA AAAA ACTGAAGGAGTTAATGATTCA TTGCTGGGGTTCCAGTCCGAAA  
ACAGGCCATCCTTCCAGGACTGCGAACC AAAA ACCAATGAAGTTTACAATCTGGTAAAGG  
ACAAGGTAGATGCTGTCTCTCCGAGGTAAAGCATTATCTGTCTCAGCACAGAAGCAGCG  
GCAGAACTTGTCTGCCAGAGAGCCAAGCCAAAGAGGCACAGAAATGGATTGCCCGAGGG  
AAACCATGGTTTCTAAAATGCTGGACCGCCTGCATTGAGGGAACCCCTCCGGACCAGTTC  
CTGGA AAATGTCCTGAGAGGCAAGCACAGGACACATCAGTTGGGCCTGCCACACCAGCAA  
GGACATCTTCTGACCCCGTGGCTGGCACTCCTCAGATTCCACATACTTTACCCCTCAGAG  
GCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCTCACC CC CAAGGAATCAGG  
GAGATGGAAGACACGGCACTCCTTGGTATCCCTGGACCCCAACCAATGACAGGGC  
CACCGGCTCTCGTCTTCAACA ACTGTTCTGAAGTGCAGATTGGGAACTACA ACTCCTTGG  
TAGCACCACCAAGAACTACTGCCTCAAGTTCGGCCAAGTATGACCAAGCACAGTTTCGGCA  
GGGGTAGGGGCTGGCAGCCCTTCCACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGA  
AGTGTGCCATTGAGCGTGGCAATAAAAAGCACGTTTTTAAGCAACCTGGACTGGCTAAGAC  
AGTCCTTGCCACTTCCCTGAAGCTCACAACATTCTGTGAGGACAGTTGGACCTACACCCAA  
ACTGACTCTTGACCCATCTCCTTAAAGTCAATAAACATAGCATGTAACTGTG

SEQ ID NO: 86\_AA744236\_H

ATGGGATCAGAGAACAGTGCTTTAAAGAGCTATACACTGAGAGAACCACCATTTACCTTA  
CCCTCTGGACTTGCTGTTTATCCCGCTGTACTGCAAGATGGCAAATTTGCTTCAGTTTTT  
GTGTATAAGAGAGAAAATGAAGACAAGGTTAATAAAGCTGCCAAGCATTGGAAGCACTT  
CGTCACCCCTTGCTTGCTAAGATTTTTATCTTGTA CTGTGGAAGCGGATGGCATTCTCTT  
GTCACTGAGCGAGTACAGCCCTTGAAGTGGCTTTGGAAACATTGTCTTCTGCAGAGGTC  
TGTGCTGGGATCTATGACATATTGCTGGCTCTTATCTTCCCTTCATGACAGAGGACACCTA  
ACACACAATAATGTCTGTTTATCATCTGTGTTTGTGAGTGAAGATGGACACTGGAAGCTA  
GGAGGAATGGAACTGTTTGTAAGTTTCTCAGGCCACACCAGAGTTTCTGAGGAGTATT

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## FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCACAACT  
CTCCCAGAGTGTCTATGGACATGCCCGGGATGCCTTTTTCATTTGGAACATTGGTGGAAAGT  
TTGCTCACAATCTTAAATGAACAGGTTTCAGCGGATGTTCTCTCCAGCTTTCAACAGACC  
TTGCACTCAACTTTGCTGAATCCCATTCCAAAATGTGCGCCAGCGCTCTGCACCTTACTA  
TCTCATGACTTCTTCAGAAATGATTTTCTGGAAGTTGTGAATTTCTTGAAAAGTTTAAACA  
TTGAAGAGTGAAGAGGAGAAAACGGAATTCTTTAAATTTCTGCTGGACAGAGTCACTGCTGC  
TTGTCAGAGGAATTGATAGCTTCAAGGTTGGTGCCTCTTCTGCTTAATCAGTTGGTGTTT  
GCAGAGCCAGTGGCTGTTAAGAGTTTTCTTCCTTATCTGCTTGGCCCCAAAAAAGATCAT  
GCGCAGGGAGAACTCCTTGCTTGCTCTCACCAGCCCTGTTCCAGTCACGGGTGATCCCC  
GTGCTTCTCCAGTTGTTTGAAGTTTCATGAAGAGCATGTGCGGATGGTGTCTGTCTCAC  
ATCGAGGCCCTACGTGGAGCACTTCACTCAGGAGCAGCTGAAGAAAGTCATCTTGCCACAG  
GTTTTGCTGGGCCTGCGTGATACTAGCGATTCCATTGTGGCAATTACTCTGCATAGCCTA  
GCAGTGCTGGTCTCTCTGCTTGGACCAGAGGTGGTTGTGGGAGGAGAACGAACCAAGATC  
TTCAAACGCACTGCCCCAAGTTTTACTAAAAATACTGACCTTTCTCTAGAAGGCGATCCA  
TTTTCTCAGCCTATTAAATTTCCCATAAATGGACTCTCAGATGTAAAAATACTTCGGAG  
GACAGTGAAAACCTCCCATCAAGTTCTAAAAAGTCTGAGGAGTGGCCTGACTGGAGTGAA  
CCTGAGGAGCCTGAAAATCAAACCTGTCAACATACAGATTTGGCCTAGAGAACCTTGATGAT  
GATGTCAAGTCCCACTGCACTACCTTGGATGTGGAAGAGTCATCTTGGGATGACTGCGAG  
CCCAGCAGCTTAGATACTAAAGTAAACCCAGGAGGTGGAATCACTGCTACAAAACCTGTT  
ACCTCAGGGGAGCAGAAGCCTATTCTGCTTTTGGCTTTCACTCACTGAAGAGTCTATGCCT  
TGGAATCAAGCTTACCCCAAAAGATTAGCCTTGTACAAAGGGGGGATGACGCAGACCAA  
ATCGAGCCGCCAAAAGTGTATCAAGAAAGGCCCTTAAGGTTCCATCAGAACTTGGT  
TTAGGAGAGGAATTCACCATTCAAGTAAAAAAGAGCCAGTAAAGATCCTGAGATGGAT  
TGGTTTGCTGATATGATCCAGAAATTAAGCCTTCTGCTGCTTTTCTTATATTACCTGAA  
CTGAGGACAGAAATGGTCCCCAAAAGGATGATGTCTCCCCAGTGATGCAGTTTCTCTCA  
AAATTTGCTGCAGCAGAAATTACTGAGGGAGAGGCTGAAGGCTGGGAAGAAGAAGGGGAG  
CTGAACTGGGAAGATAATAACTGGTGA

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AGCGGCCGCGGGGGCGGCGGAGGATATGGAGTAAAGCCAGAGTCAGTGGCCAGGCACGAA  
GGCAGAGCAGGAACAGCCAGGAGGCGTTTATTAGGGGGGCGGGGGGAAAGAGCCCCAGCA  
CCGCCCCCTCTGGAAGAAGGAAGAGGTAACTATACTACCCAATATTGCAGCCATGGAGT  
CCATGCTTAATAAATTGAAGAGTACTGTTACAAAAGTCACAGCTGATGTCACTAGTGCGG  
TAATGGGAATTCCTGTCACTAGAGAATTTGATGTTGGTTCGACACATTGCCAGTGGTTGCA  
ATGGGCTAGCTTGGAAAGATTTTAAATGGCACAAAAAAGTCAACAAAGCAGGAAGTGGCAG  
TTTTTGCTCTTTGATAAAAACTGATTGACAAGTATCAAAAATTTGAAAAGGATCAAATCA  
TTGATTCTCTAAACGAGGAGTCCAACAGTTAACTCGGCTTCGACACCCCTCGACTTCTTA  
CTGTCCAGCATCCTTTAGAAGAATCCAGGGATTGCTTGGCATTTTGTACAGAACCAGTTT  
TTGCCAGTTTAGCCAATGTTCTTGGTAACTGGGAAAATCTACCTTCCCCTATATCTCCAG  
ACATTAAGGATTATAAACTTTATGATGTAGAAACCAAATATGGTTTGCTTCAGGTTTCTG  
AAGGATTGTCAATTCTTGATAGCAGTGTGAAAATGGTGCATGGAAATATCACTCCTGAAA  
ATATAATTTGAATAAAAGTGGAGCCTGGAAAATAATGGGTTTTGATTTTTGTGTATCAT  
CAACCAATCCTTCTGAACAAGAGCCTAAATTTCTTGTAAAGAATGGGACCCAAATTTAC  
CTTCATTGTGTCTTCCAAATCCTGAATATTTGGCTCCTGAATACATACTTTCTGTGAGCT  
GTGAAACAGCCAGTGATATGTATTCTTTAGGAACTGTTATGTATGCTGTATTTAATAAAG  
GGAAACCTATATTTGAAGTCAACAAGCAAGATATTTACAAGAGTTTCAGTAGGCAGTTGG  
ATCAGTTGAGTCGTTTAGGATCTAGTTCACTTACAAATATACCTGAGGAAGTTTCGTGAAC  
AGATTCCTTCTTTGATGATGTTGGTGCAGTAACACTGCAATATTTTGATACCTTATTCC  
AAAGAGATAATCTTCAGAAATCACAGTTTTTCAAAGGACTGCCAAAGGTTCTACCAAAC

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## FIGURE 2RRR

TGCCCAAGCGTGTTCATTGTGCAGAGAATTTTGCTTGTGTTGACTTCAGAATTTGTAAACC  
CTGACATGGTACCTTTTGTGTTTGCCTAATGTTCTACTTATTGCTGAGGAATGCACCAAAG  
AAGAATATGTCAAATTAATTCTTCTGAACTTGGCCCTGTGTTTAAGCAGCAGGAGCCAA  
TCCAGATTTTGTGTTAATTTTCTTACAAAAAATGGATTGCTACTAACCAAAACCCCTCCTG  
ATGAGATAAAGAACAGTGTCTACCCATGGTTTACAGAGCACTAGAAGCTCCTTCCATTC  
AGATCCAGGAGCTCTGTCTAAACATCATTTCCAACCTTTGCAAATCTTATAGACTACCCAT  
CCATGAAAAACGCTTTGATACCAAGAATTAATAATGCTTGCTACAAACATCTTCCCTTGC  
GGTTCGTGTAAATTCATTAAACAACATTGGAGCAGACCTTCTGACTGGCAGTGAGTCCG

SEQ ID NO: 88\_AA278842\_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCCCCGGCTCGGGCGGCCGGAG  
GACCCGGAGCTAAGGCGCCCCGAACCCGCGGCGGGTGGGGACGATGTGGTTCTTTGCCC  
GGGACCCGGTCCGGGACTTTCCGTTTCGAGCTCATCCCGGAGCCCCAGAGGGCGGCCTGC  
CCGGGCCCTGGGCCCTGCACCGCGGCCGCAAGAAGGCCACAGGCAGCCCCGTGTCCATCT  
TCGTCTATGATGTGAAGCCTGGCGCGGAAGAGCAGACCCAGGTGGCCAAAGCTGCCTTCA  
AGCGCTTCAAACTCTACGGCACCCCAACATCCTGGCTTACATCGATGGACTGGAGACAG  
AAAAATGCCTCCACGTCTGTGACAGAGGCTGTGACCCCGTTGGGAATATACCTCAAGGCGA  
GAGTGGAGGCTGGTGGCCTGAAGGAGCTGGAGATCTCCTGGGGGCTACACCAGATCGTGA  
AAGCCCTCAGCTTCTGGTCAACGACTGCAGCCTCATCCACAACAATGTCTGCATGGCCG  
CCGTGTTCTGTGGACCGAGCTGGCGAGTGGGAAGCTTGGGGGCTGGACTACATGTATTCCG  
CCCAGGGCAACGGTGGGGGACCTCCCCGCAAGGGGATCCCCGAGCTTGAGCAGTATGACC  
CCCCGGAGTTGGCTGACAGCAGTGGCAGAGTGGTCAGAGAGAAGTGGTCAGCAGACATGT  
GGCGCTTGGGCTGCCTCATTTGGGAAGTCTTCAATGGGCCCCTACCTCGGGCAGCAGCCC  
TACGCAACCCTGGGAAGATCCCCAAAACGCTGGTGGCCCCATTACTGTGAGCTGGTGGGAG  
CAAACCCCAAGGTGCGTCCCAACCCAGCCCGCTTCTGCAGAACTGCCGGGCACCTGGTG  
GCTTCATGAGCAACCGCTTTGTAGAAACCAACCTCTTCTGGAGGAGATTAGATCAAAG  
AGCCAGCCGAGAAGCAAAATTTCTTCCAGGAGCTGAGCAAGAGCCTGGACGCATTCCCTG  
AGGATTTCTGTGCGGCACAAGGTGCTGCCCCAGCTGCTGACCGCCTTCGAGTTCGGCAATG  
CTGGGGCCGTTGTCTTACGCCCCCTCTTCAAGGTGGGCAAGTTCTTGAGCGCTGAGGAGT  
ATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGC  
GCATCCGCCTCCTGCAGCAGATGGAGCAGTTTATCCAGTACCTTGACGAGCCAACAGTCA  
ACACCCAGATCTTCCCCACGTCGTACATGGCTTCTTGACACCAACCCTGCCATCCGGG  
AGCAGACGGTCAAGTCCATGCTGCTCCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATG  
TGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACAGGGCCCCATCCGCT  
GCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGACACA  
GGGTCTTACCTCTGCCTTACGCCGAGCCACTAGGGACCCGTTTGACCCGTCCCGGGTTG  
CGGGTGTCTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCAGA  
AGATCCTGCCTGTGCTCTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGG  
CCTTCAAGGCCATTCCGAGCTTCTGTCCAAATTTGGAGTCTGTGTGCGAGGACCCGACCC  
AGCTGGAGGAAGTGGAGAAGGATGTCCATGCAGCCTCCAGCCCTGGCATGGGAGGAGCCG  
CAGCTAGCTGGGCAGGCTGGGCCGTGACCGGGTCTCCTCACTCACCTCCAAGCTGATCC  
GTTTCGCACCCAACCACTGCCCCAACAGAAACCAACATTCCCCAAAGACCCACGCCTGAAG  
GAGTTCCTGCCCCAGCCCCCACCCTGTTCTTGCCACCCCTACAACCTCAGGCCACTGGG  
AGACGCAGGAGGAGGACAAGGACACAGCAGAGGACAGCAGCACTGCTGACAGATGGGACG  
ACGAAGACTGGGGCAGCCTGGAGCAGGAGGCCGAGTCTGTGCTGGCCAGCAGGACGACT  
GGAGCACCGGGGGCCAAGTGAGCCGTGCTAGTCAGGTGAGCAACTCCGACCACAAATCCT  
CCAAATCCCCAGAGTCCGACTGGAGCAGCTGGGAAGCTGAGGGCTCCTGGGAACAGGGTT  
GGCAGGAGCCAAGCTCCCAGGAGCCACCTCCTGACGGTACACGGCTGGCCAGCGAGTATA  
ACTGGGGTGGGCCAGAGTCCAGCGACAAGGGCGACCCCTTCGCTACCCTGTCTGCACGTC  
CCAGCACCCAGCCGAGGCCAGACTCTTGGGGTGAGGACAACCTGGGAGGGCCTCGAGACTG

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## FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCGGAAGAAGCGCGAGGAGCGGCGGGGAGA  
TGGAGGCCAAACGCGCCGAGAGGAAGGTGGCCAAGGGCCCCATGAAGCTGGGAGCCCGGA  
AGCTGGACTGAACCGTGGCGGTGGCCCTTCCCGGCTGCGGAGAGCCCCGCCACAGATGT  
ATTTATTGTACAAACCATGTGAGCCTGGCCGGCCAGCCAGGCCATCTCACGTGTACATA  
ATCAGAGCCACAATAAATTCTATTTTAC

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ATGGCCCTTCATGGAGAAGCCGCCAGCCGGCAAGGTGCTGCTGGACGACACGGTGCCGCTG  
ACAGCAGCCATCGAGGCGAGCCAGAGCCTGCAGTCCCACACGGAATATATTATTCGAGTG  
CAAGGAGGAATTTCTGTGAAAACAGCTGGCAGATTGTTAGAAGATACAGTGACTTTGAT  
TTGCTTAACAACAGCTTACAGATTGCAGGCCTAAGTCTACCTCTTCCCTCCCAAAAATTTG  
ATTGGTAACATGGATCGTGAATTCATAGCTGAAAGGCAGAAAGGTCTTCAGAACTATCTC  
AACGTGATCACAACAAATCATATCTTGTCTAATTGTGAGCTGGTTAAGAAGTTTTTAGAT  
CCAAACAACCTATTCCGCAAACTATACTGAGATTGCCTTGCAACAGGTTTTCCATGTTCTTC  
CGATCAGAGCCAAAGTGGGAGGTGGTGGAACCTTTGAAAGACATAGGTTGGAGAATAAGG  
AAGAAATATTTCTTGATGAAGATTAAAAATCAGCCAAAGGAACGGCTAGTGTTAAGCTGG  
GCTGACCTTGCGCCAGACAAGTATTTGTGAGATAAAGATTTTCAGTGTCTAATCAAACCTT  
CTGCCTTCTTGTGTTGACCCCTTACATCTATCGGGTTACCTTTGCCACAGCTAATGAATCC  
TCAGCGTTGCTAATTAGGATGTTTAAACGAAAAGGGAACATTGAAGGATCTGATCTACAAG  
GCAAAACCAAAAGACCCATTTCTAAAGAAGTACTGCAACCCTAAGAAGATTCAGGGCCTG  
GAATCCAGCAAATAAAAAACATATGGACGGCAAATATTAGAGGTACTGAAGTTTCTTCAT  
GACAAGGGATTCCCTTATGGGCATCTTCACGCCTCCAATGTGATGCTCGATGGGGACACT  
TGCCCGCTGCTGGACCTTGAGAATTCCTTATTGGGCCTGCCTTCTTCTACCGATCTTAT  
TTTTTACAATTCAGGAAAATCAATACATTGGAAAGTGTGGATGTCCACTGCTTTTGCCAC  
TTACTGTATGAAATGACTTATGGACGACCGCCAGACTCGGTGCCTGTGGACTCCTTCCCT  
CCTGCCCCGTCCATGGCTGTGGTGGCCGTGTTGGAGTCTACGCTGTCTTGTGAAGCCTGT  
AAAAATGGCATGCCTACCATCTCCCGCTCTTACAGATGCCATTATTCAGCGATGTTTTA  
CTAACCACTTCTGAAAAACACAGTTTAAAGATCCCTACAAAGTTAAAAGAGGCATTGAGA  
ATTGCCAAAGAATGTATAGAGAAGAGACTAATTGAGGAACAGAAACAGATTACCCAGCAT  
CGAAGACTGACAAGAGCTCAGTCCCACCATGGATCTGAGGAGGAAAGAAAAAAGAAAG  
ATTTTAGCTCGAAAGAAGTCAAAACGATCTGCTCTTGAAAATAGTGAAGAGCATTACAGCG  
AAGTACAGCAACTCCAATAATTACAGCAGGATCTGGGGCCAGCTCACCTCTCACGTCCCCG  
TCATCGCCAACCTCCACCTCTACATCAGGGATATCTGCATTACCTCCACCTCCTCCACCT  
CCACCACCACCAGCAGCTCCCTTGCCCTCCTGCGAGCACCGAGGCACCTGCCCAGCTCTCG  
TCTCAGGCTGTGAATGGCATGAGCCGAGGGGCTTGCTCAGCTCCATCCAGAATTTCCAA  
AAAGGAACTTTGAGGAAAGCCAAACCTGTGATCACAGTGCTCCGAAGATCGGCTGAAGCT  
TCCTGTTTACACTTGAGGGGAAAAGTTCTTTTTTTATTCTACTCACCCCTACCCCCAAC  
TACCCTCTTCTGGGAAAGTAATTGCTGAGCCAGTACAGCCACAAACAGTACTATTTTGC  
AGATGCTCATGTAAGCAGCTTTTCGAGAGAAATAATTCTTTAAGCAGAATAAAGTTAGGC  
TGGCATGCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 90\_AA425725\_H

ATGAGCGCCAGCACGGGCGGTGGTGGGGACAGCGGCGGCAGCGGCGGCAGTAGCAGCAGC  
TCACAGGCCCTCTGCGGGCCCGAGTCTTCCGGGCTCCGAACTAGCCCTGGCCACACCGGTG  
CCTCAGATGCTGCAGGGCCTTCTGGGCTCCGACGACGAGGAACAGGAAGACCCCAAAGAC  
TACTGCAAGGGCGGCTACCAACCTGTGAAGATCGGCGACGTGTTCAATGGGCGGTACCAC  
GTGGTGCGCAAACCTGGGCTGGGGCCACTTCTCCACCGTCTGGCTCTGCTGGGACATCCAG  
CGCAAGCGCTTTGTGGCCCTCAAAGTGGTGAAGAGTGCAGGGGCATTACACGGAGACAGCT  
GTGGATGAGATCAAGCTCCTGAAATGTGTCCGGGACAGCGACCCCAAGTACCCCAAAAGA  
GAGACCATTGTCCAGCTCATTGATGACTTCAGGATCTCAGGAGTCAATGGAGTCCATGTG

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## FIGURE 2TTT

TGCATGGTGTCTGGAGGTGCTGGGCCACCAGCTCCTCAAATGGATCATCAAGTCCAACTAC  
CAGGGCCTGCCCCGTGCCCTGCGTGAAGAGCATCGTGAGGCAGGTGCTGCACGGCCTGGAC  
TACCTCCACACCAAGTGCAAGATCATCCACACGGACATCAAGCCCCGAGAACATCTTGCTG  
TGTGTGGGGGACGCTTACATCAGGCGCCTGGCTGCCGAGGCCACGGAGTGGCAACAGGCA  
GGGGCGCCGCCCCCTCCCGCTCCATAGTCAGCACTGCCCCCAGGAGGTCTTGACCGGT  
AAGCTGTCCAAAAACAAGAGGAAGAAGATGAGGCGCAAACGGAAAACAGCAGAAGCGGCTG  
CTGGAGGAGCGGCTGCGGGACCTGCAGAGGCTGGAGGCCATGGAGGCTGCCACCCAGGCT  
GAGGACTCTGGCTTGAGACTAGACGGGGGACGCGGCTCCACATCCTCTTCAGGCTTCTCC  
GGCTCCCTCTTCTCTCCTGCCTCCTGCTCCATCCTCTCCGGCTCGTCCAATCAGCGAGAG  
ACCGGGGGCCTCCTGTGCGCTAGCACACCATTCGGTGCCTCGAACCTCCTGGTGAACCCC  
CTGGAGCCCCAAAATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGC  
TGGGTGCACAAGCACTTCACGGAAGACATCCAGACTCGGCAGTACCGGGCCGTCGAGGTG  
CTGATCGGCGCCGAATACGGCCCCCGGCAGACATCTGGAGCACAGCCTGCATGGCCTTC  
GAGCTGGCCACTGGTGACTIONCTGTTTCGAGCCGCATTCTGGAGAAGACTACAGTCGTGAT  
GAGGACCACATCGCTCACATAGTGGAGCTTCTGGGGGACATCCCCCAGCCTTCGCCCTC  
TCAGGCCGCTATTCCCGGGAGTTCTTCAACCGGAGAGGAGAGCTGCGGCACATCCACAAT  
CTCAAGCACTGGGGCCTGTACGAGGTACTIONTATGGAAAAGTACGAGTGGCCCCCTAGAGCAG  
GCCACACAGTTACGCGCCTTTCTGCTGCCCATGATGGAGTACATCCCCGAAAAGCGGGCC  
AGTGCCGCTGACTGCCTCCAGCACCCCTGGCTCAACCCCTAG

SEQ ID NO: 91\_SGK022\_H

TCTGGCCCTGTCCCTCCCCACCACCCGCGCTGTGTCCAGACAGAGAATGTTCTAACGCT  
GGGGGCGGCTGCGGATGAAGTCCTTGGGGAGAAAAGGAGCAGGCCAAGGGCGATGGTGGA  
GTAGAGCTGCCTCTCAGAGGCAGCATGAGCTGAGAGGGTGATAGGAAGGCGGCGCTAGAC  
AGCATGGAGGACTTTCTGCTCTCCAATGGGTACCAGCTGGGCAAGACCATTGGGGAAGGG  
ACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAAACACCAAAGAAAAGTGGCAATTAAA  
GTTATAGACAAGATGGGAGGGCCATCAGAGTTTATCCAGAGATTCTCCCTCGGGAGCTC  
CAAATCGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCT  
GCCGACGGGAAAACTGCCTGGTGTATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGC  
GTGCTGAATGGGGGGCCACTGCCTGAAAGCCGGGGCCAAGGCCCTCTTCCGTGAGATGGTT  
GAGGCCATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAAC  
GCCTTGTGTCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCC  
AAGTCACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCGAG  
GTGCTGCAGGGCATTCCCCACGATAGCAAAAAGGTGATGTCTGGAGCATCCCCAAGATGCTG  
CTGTATGTATGCTCTGTGCCAGCCTACCTTTTGACGACACAGACATCCCCAAGATGCTG  
TGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATCTGAGCATCTCGGCCGATTGCCAG  
GACCTGCTCAAGAGGCTCCTGGAACCCGATATGATCCTCCGGCCTTCAATTGAAGAAGTT  
AGTTGGCATCCATGGCTAGCAAGCACTTGATAAAAGCAATGGCAAGTGCTCTCCAATAAA  
GTAGGGGGAGAAAGCAA

SEQ ID NO: 92\_AA060026\_M SGK022\_M

CAGACGGAGAATGTTCTAGCCCTGGAGGCAGCTGTGAATGAAGTCCTTGCGGGGAAAAGA  
AGCAGGCCGAGGGCGATGGTGGAGTAGAGCTGCCTCGCAGAGGCAGCATGAGCTGAGAGG  
GTGACAAGAAGGAGGCGCTACACAGCATGGAGGACTTTCTACTCTCCAATGGGTATCAGC  
TGGGCAAGACCATTGGGGAAGGGACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAAAC  
ATCAAAGAAAAGTGGCAATTAAATATAGACAAGATGGGAGGGCCAGAAGAGTTTATCC  
AGAGATTCCTGCCTCGTGAGCTCCAGATTGTCCGTACCCTGGACCACAAAACATCATCC  
AGGTGTATGAGATGCTGGAGTCAGCAGATGGAAAAATCTACCTGGTGTATGGAAGTGGCTG  
AGGGAGGGGATGTCTTTGACTGTGTGCTGAACGGAGGGCCACTTCCCGAGAGCCGGGCCA  
AGGCCCTCTTCCGCCAGATGGTTGAGGCTATTGCTATTGCCATGGCTGTGGCGTGGCCC

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## FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTCAGGGCTTCAACCTGAAGCTGACCGACT  
TTGGCTTTGCCAAGGTGCTACCCAAGTCACGCAGGGAGCTGAGCCAGACCTTCTGTGGCA  
GCACAGCCTATGCCGCCCCCTGAGGTGCTACAGGGCATAACCCCATGATAGCAAGAAAGGTG  
ATGTCTGGAGCATGGGTGTGGTCCTGTATGTAATGCTCTGTGCAAGTCTACCTTTTGATG  
ACACAGATATCCCCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATT  
TGGGCATCTCAACCGAATGCCAGGACCTGCTCAAGCGGCTCCTGGAACCAGACATGATAC  
TCCGGCCTTCAATCGAAGAAGTTAGTTGGCACCCATGGCTAGCAAGCACTTGATAAAAGC  
AATGGCAAGTCCTCCCCAATAAAGTAGGGGGAGAAAGCAAACCTG

SEQ ID NO: 93\_AA399669\_H

CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCACTTCATTCTCAA  
GTTTTGTGGCCAACGATGGATAGGAGGTGGATTGTGATGTATTTCGGAACATGGGACCTTG  
AGGAGTTCCGTAACCAAAAGGAGAAAGTAACAACAGCCAGTGAGACAAAAGAACTGCT  
TCTCTTTCTTTCCCCCTCCAAGTTCCTAGTGAGGGCTGAGTCCAGCATCCCAGACTCGT  
GTGACTATATAGGCAAGCATTGTTGGGACCTACTTCACTTTGATACCCTAGCCTTCAGCAG  
CTCAAGGTGTTGGCCTTTGGATAGGAGGCTTCCAAGTAGTAAAGCTCCCTGCTCTCAGCA  
AGCCCAACACCATGGGGAAGGGAGATGTCTTAGAGGCAGCACCAACCACCACAGCCTACC  
ATTCCCTCATGGATGAATATGGTTATGAGGTGGGCAAGGCCATTGGCCATGGCTCCTATG  
GGTCGGTATATGAGGCTTTCTACACAAAGCAGAAGGTTATGGTGGCAGTCAAGATCATCT  
CAAAGAAGAAGGCCTCTGATGACTATCTTAACAAGTTCCTGCCCCGTGAAATACAGGTAA  
TGAAAGTCTTGCGGCACAAGTACCTCATCAACTTCTATCGGGCCATTGAGAGCACATCTC  
GAGTATACATCATTCTGGAACTGGCTCAGGGTGGTGTATGTCTTGAATGGATCCAGCGCT  
ACGGGGCCTGCTCTGAGCCCCTTGCTGGCAAGTGGTTCTCCCAGCTGACCCTGGGCATTG  
CCTACCTGCACAGCAAGAGCATCGTGACCCGGGACTTAAAGTTGGAGAACCTGTTGCTGG  
ACAAGTGGGAGAATGTGAAGATATCAGACTTTGGCTTTGCCAAGATGGTGCCTTCTAACC  
AGCCTGTGGGTTGTAGCCCTKCTTACCGCCAAGTGAAGTCTTTTCCCACCTCAGCCAGA  
CTTACTGTGGCAGCTTTGCTTACGCTTGCCCAGAGATCTTACGAGGCTTGCCCTACAACC  
CTTTCTGTCTGACACCTGGAGCATGGGCGTCATCCTTTTACACTCTAGTGGTCGCCCATC  
TGCCCTTTGATGACACCAATCTCAAAAAGCTGCTAAGAGAGACTCAGAAGGAGGTCACTT  
TCCCAGCTAACCATACCATCTCCCAGGAGTGCAAGGTCCAAGTCTGCTCATTGCCTGTGTGG  
CACAATGGAGAAAACTCAGGCAAGACCTCTCTCTCCCCTGCTCTAGAACCTGATCCTCC  
AGATGCTACGCCAAGCCACTAAGCGTGCCACCATTCTGGACATCATCAAGGATTCTCTGGG  
TGCTCAAGTTCAGCCTGAGCAACCCACCCATGAGATCAGGCTGCTTGAGGCCATGTGCC  
AGCTCCACAACACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA  
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAA  
AAATAAATCTAAGTCTGATTTAGTTTCATCAAAAAA

SEQ ID NO: 94\_AA758539\_H

GACCATTGACAGCGCTCCGGTAGTGTAATGAGGACAAATGCCTGCTGGCCACATGACGG  
GGGGATGTAGACGGCAGCGGCCAGTCTGCTCCTGGCACCATTGGACGATGCCACAGTCCT  
AAGGAAGAAGGGTTACATCGTAGGCATCAATCTTGGCAAGGGTTCCTACGCAAAAGTCAA  
ATCTGCCTACTCTGAGCGCCTCAAGTTCAATGTGGCTGTCAAGATCATCGACCGCAGGAA  
AACACCTACTGACTTTGTGGAGAGATTCTTCTCCTCGGGAGATGGACATCCTGGCAACTGT  
CAACCACGGCTCCATCATCAAGACTTACGAGATCTTTGAGACCTCTGACGGACGGATCTA  
CATCATCATGGAGCTTGGCGTCCAGGGCGACCTCCTCGAGTTCATCAAGTGCCAGGGAGC  
CCTGCATGAGGACGTGGCAGCAAGATGTTCCGACAGCTCTCCTCCGCCGTCAAGTACTG  
CCAGGACCTGGACATCGTCCACCGGGACCTCAAGTGCGGAGAACCTTCTCCTCGACAAGGA  
CTTCAACATCAAGCTGTCTGACTTTGGCTTCTCCAAGCGCTGCCTGCGGGACAGCAATGG  
GCGCATCATCCTCAGCAAGACCTTCTGCGGGTCCGACGATATGCAGCCCCCGAGGTGCT  
GCAGAGCATCCCCTACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

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## FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT  
CCAGAAGGAGCACCGTGTGGACTTCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA  
CCTCATCTACCGCATGCTGCAGCCCCGACGTGAGCCAGCGGCTCCACATCGATGAGATCCT  
CAGCCACTCGTGGCTGCAGCCCCCAAGCCC~~AA~~AGCCACGTCTTCTGCCTCCTTCAAGAG  
GGAGGGGGAGGGCAAGTACCGCGCTGAGTGCAAACCTGGACACCAAGACAGGCTTGAGGGCC  
CGACCACCGGCCCCGACCACAAGCTTGGAGCCAAACCCAGCACCGGCTGCTGGTGGTGCC  
CGAGAACGAGAACAGGATGGAGGACAGGCTGGCCGAGACCTCCAGGGCCAAAGACCATCA  
CATCTCCGGAGCTGAGGTGGGGAAAGCAAGCACCTAGCATGACAATGGCCCCGTTGTGTG  
TGGTGGGGGTCGGGGTTGGGGGGCATGGTGCAGTCGGCCTTACGTAAACTAAGTAGGCA  
GGTAGGATCTGAAGAAGGCACAGGTGCAAGTAAATTCGTCAATTAACCACTATTTTGA  
TT

SEQ ID NO: 95\_AA883975\_H

ATGTCGGGAGACAACTTCTGAGCGAACTCGGTTATAAGCTGGGCGCACAAATTGGAGAG  
GGCAGCTACTCCAAGGTGAAGGTGGCCACATCCAAGAAGTACAAGGGTACCGTGGCCATC  
AAGGTGGTGGACCGGCGGCGAGCGCCCCGGACTTCGTCAACAAGTTCCTGCCGCGAGAG  
CTGTCCATCCTGCGGGGCGTGCGACACCCGCACATCGTGCACGTCTTCGAGTTCATCGAG  
GTGTGCAACGGGAACTGTACATCGTGATGGAAGCGGCCGCCACCGACCTGCTGCAAGCC  
GTGCAGCGCAACGGGCGCATCCCCGGAGTTCAGGCGCGCGACCTCTTTGCGCAGATCGCC  
GGCGCCGTGCGCTACCTGCACGATCATCACCTGGTGCACCGCGACCTCAAGTGCGAAAAC  
GTGCTGCTGAGCCCGGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG  
GCCCATGGCTACCCAGACCTGAGCACCACTACTGCGGCTCAGCCGCCTACGCGTCACCC  
GAGGTGCTCCTGGGCATCCCCACGACCCCAAGAAGTACGATGTGTGGAGCATGGGCGTC  
GTGCTCTACGTGATGGTCAACGGGTGATGCCCTTCGACGACTCGGACATCGCCGGCCTG  
CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC  
AAGGCCCTGATCGCCGAGCTGCTGCAGTTCAGCCCCGTCCGCCAGGCCCTCCGCGGGCCAG  
GTAGCGCGCAACTGCTGGCTGCGCGCCGGGGACTCCGGCTAG

SEQ ID NO: 96\_AA905446\_H

CTGGTAGAGAACAGGGGCTGGTGCCAAGGCCCATGGAGATGAGAAAACGGAAGACAGGGA  
TCATGGAAAGAAATTGTGGGGTCAGGGGACAGTGGCGGGAGGAGCTGGCTCACCACCCTGT  
GGACAAATCAGGCCTTATAATTTGTGATTCTGTGGCTTTGTCTAAAAGTCCATAAAGCAC  
CTTGATATCCAGTCTCACAGACTGCTCACAACAGTCCACAAGGCTGGTGGGGAGTGCTTC  
TTTTGAATGATATACTAACGACAAAAATAATAGAAGTGAACATTCTTTGCAATGTCCAAG  
CAGCTAGACACACTTAAGACCATTAAGAAAGCCAAGAAATAAGACCCAGACAAGGTGGGC  
AGAAGTTGGAAGGCAGGAGACAGGTGTGAGGAGGTGGGCCTTTCTGATCTGCCAGCCCAT  
CTCTCCTCCCCTTACTTCCTCAGAGTTTATCCAGAGATTCTCCTCCCTCGGGAGCTCCAAAT  
CGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCTGCCGA  
CGGGAATAATCTGCCTGGTGATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGCGTGCT  
GAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTGAGTGGTTGAGGC  
CATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAACGCCTT  
GTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCAAGTC  
ACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAGGTGCT  
GCAGGGCATTTCCNNCAAGATGCTGTGGCAGCAGCAGAAGGGGTGTCTTCCCCACTCA  
TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT  
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA  
GCAATGGCAAGTGCTCTCCAATAAAGTAGGGGGAGAAAGCAAACCC



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## FIGURE 2WWW

SEQ ID NO: 97\_H29974\_H

TTACAGCCTGTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCAGTGGC  
CGGGCGCAGCGGGGCCCGGGTGGCGGTCAAGAAGATCCGCTGCGACGCCCCGAGAACGT  
GGAGCTGGCGCTGGCTGAATTCTGGGCCCTCACCAGCCTCAAGCGGCGCCACCAGAACGT  
CGTGCACTTTGAGGAGTGGTCCTGCAGCGCAATGGGTTAGCCCAGCGCATGAGTCACGG  
CAACAAGAGCTCGCAGCTTTACCTGCGCCTGGTGGAGACCTCGCTGAAAGGAGAAAGGAT  
CCTGGGTTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTCTATGGAGTTCTGTGAAGGTGG  
AGACCTGAATCAGTATGTCCTGTCCCGGAGGCCAGACCCAGCCACCAACAAAAGTTTCAT  
GCTACAGCTGACGAGCGCCATTGCCTTCTTGACAAAAACCATATTGTGCACAGGGACCT  
GAAGCCAGACAACATCCTCATCAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA  
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGA  
CAACAAAATGTGAATGTGAATAAGTACTGGCTGTCTCAGCCTGCGGTTCCGACTTCTA  
CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG  
CATTATCATCTGGGCAATGATAGAAAGAATCACTTTTATTGACTCTGAGACCAAGAAGGA  
GCTCCTGGGGACCTACATTAAACAGGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCT  
AGAAAACCCAAAGATGGAGTTGCACATCCCCAAAAACGCAGGACTTCCATGTCTGAGGG  
GATCAAGCAGCTCTTGAAAGATATGTTAGCTGCTAACCACAGGACCGGCCTGATGCCTT  
TGAAGTTGAAACCAGAATGGACCAGGTACATGTGCTTAAATTCAGGGCTAAGCAT  
TTTGGGTGATTTTAACTAGGTGATTCCTCGGGACCCACAGTCTCACCACGTCTCCTCC  
AGAGGACGGCAGAGGGTACAGGTGGTGGCCTGGCCGCTTGGCGATCTCCCGACAGCTGGA  
TCCGGCAATGTGAAGCTTTTGTGGGTTTCCCGCTTCTTTTTAGTTTTGCTTTATTN  
TNCCCTTTTCTTTTCTTTTTTNTTNNCCACNTNCCTTTTTTTAAATTTAAACCATTGAG  
ACTTCAGAAAGAGCAGGACACAATGCTGTGGACAGGCACCAATTTCTTTAAAGAAATTCAA  
TGTGGGCAAGGCATATGTGTAAATTTCACTTTTACTTTTTATAAGGGGTTAGGGAGCTAT  
TTTTGGTTTTGTCTTCACTTTCCCTCTGTCTTCTTTATACTTTTCTCAGTTCTAC  
TTATGACACCTCACTTCCCTAGAGAAGGCCTGCCTCCCCATAGGGAATCTGGGGGTANCT  
TCTGGAACGGGGCGTGAGGANACAAGGAGCCTCTGGGCCACNCCTCCCTACCAGATGCAG  
GAACTCCTGGACTCCTTGGTGGGCTGGCCCTGGCTAGCCCTTGGGCCTCGGAGATGATCA  
GAGGTGAAGAACCGCC

SEQ ID NO: 98\_AA498104\_M H29974\_M

CCGTTGCTGCTCCCCCGCCCCCGCAGCCATGGAAACGGGGAAAGAGAACGGAGCCCGC  
AGAGGGACAAAAAGCCCGGAGCGGAAAAGGCGAAGCCAGTCCAGCGGGTACTGTGCGAG  
AAGCTGAGGCGCGCGGCCAGGCCATGGATCCGGCTGGGGCCGAGGTCCCGGGCGAGGCC  
TTCTTGGCCCGCGCGGCCGGATGGCGGCGGCGGGGATGTTCTGACGCGCCGCTAC  
AGCCTCTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCTGTGGCTGGG  
CGCAGTGGGGCCAGGGTGGCAGTCAAGAAGATCCGCTGCGACGCTCCCGAGAACGTGGAG  
TTGGCACTAGCAGAATTCTGGGCCCTCACCAGTCTCAAGCGGCGGCACCAGAATATCGTG  
CAGTTTGAGGAGTGCCTCTACAGCGCAACGGGTAGCCCAGCGCATGAGTCACGGCAAC  
AAGAACTCACAGCTTTACCTGCGCCTGGTGGAGACCTCGCTCAAAGGAGAAAGGATCCTG  
GGCTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTCTATGGAGTACTGTGAAGGTGGAGAC  
CTCAATCAGTATGTCTGTCCCGGAGACCTGACCCAGCCACCAACAAAAGTTTCATGCTA  
CAGCTTACAAGCGCCATTGCCTTCTGTCATAAAAAACCATCGTGCACAGGGACCTAAAG  
CCAGACAACATCCTGATCACAGAGCGGTCTGGCACCCCCATCCTCAAGGTGGCAGACTTT  
GGACTGAGCAAGGTCTGTGCAAGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGATAAC  
AAAAATGTGAATGTGAATAAATACTGGCTGTCTCAGCTTGTGGCTCAGACTTCTACATG  
GCTCCCGAAGTCTGGGAGGGACACTATACAGCCAAGGCGGACATCTTTGCTCTGGGCATT  
ATCATCTGGGCAATGATAGAAAGAATTACCTTTATTGACTCTGAAACCAAGAAGGAGCTC  
CTGGGGACCTACATTAAAGCAAGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCTAGAA  
AACCCAAAGATGGAGTTGCATATCCCCAGAAACGTAGGACTTCCATGTCTGAGGGGGTCT



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## FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA  
CTTGAAACCCGAATGGACCAGGTACATGTGCTGCTTAAACTCCAGGGCTGAACGTCTTG  
GGTGTTTTAAACTAGGTGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA  
TGGCAGAGGGTACAGGTGGTGGTGTATCTCTGACAGCTGGACCTCCCAACAATGTGAAGCT  
CACGCTTGGGCTGCCACTCTACCCTTCTCTTCTCCTTCAGTAGAATAATAATTGTTTT  
TCTAAACATTAAACCATCAAGACTTCTGAAGAGCAGAAGGCTACACTCTG

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CGRCCGCGCTACGGAAAGCCGGAGGGGGCGGGGCCGTGCGCGTAAGGGGGTGTGTCCGC  
GCGCACCACGGGGGCGCGCGCCGGCTGCTGACTGGAGGCGGCGGAGCGGAGGCGCGAGC  
TGCCCGATAATGGCGGCCTGCAGAGCCCATGAGAGGGAGAAGCGGCAGCGTCTACCCTGA  
GAAACCTCGACCTTGAAGATGGTGTAGTAGCCAGCCAAAGTACGATCTAATACGGGAGGTA  
GGCCGAGGTAGTTACGGTGTGTGTATGAAGCAGTCATCAGAAAGACCTCTGCACGGGTG  
GCAGTGAAGAAAATTGATGTACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC  
TGGGCACTAAGCAGTATCAAGAGCCAACATCCAAATGTGATTCACTTGGAGGAATGCATC  
CTACAAAAGGATGGGATGGTGCAAAGATGTCCCACGGCTCTAATTCTTCCCTTTATTTA  
CAGCTTGTAGAACTTCATTAAAAGGAGAAATTGCCTTTGATCCCAGAAGCGCCTATTAT  
TTGTGGTTTGTGATGGATTTTGTGACGGAGGAGATATGAATGAGTATCTGTTGTCCAGG  
AAGCCCAATCGTAAACTAACACCAGCTTCATGCTTCAGCTGAGCAGTGCCCTGGCTTTC  
TTGCATAAAAACCAGATCATCCACCGAGATCTTAAGCCTGATAACATCCTGATTTCTCAA  
ACCAGGTGGGATACCAGTGACTTGGACCTACCCTCAAAGTGGCTGATTTTGGTCTAAGT  
AAAGTTTGTTCAGCCTCTGGGCAGAACCCAGAAGAACCTGTGAGTGTAACAAGTGTTC  
CTTTCCACAGCATGTGGAACAGATTTTACATGGCTCCTGAAGTTTGGGAAGGACATTAC  
ACAGCAAAAGCTGACATCTTTGCTCTGGGGATTATCATCTGGGCAATGCTGGAAGGATC  
ACATTATAGACACAGAGACAAAGAAGGAACCTTGGGGAGTTATGTAAAACAAGGAAC  
GAGATTGTGCCTGTTGGGAGGCACTTCTGGAATAATCCCAAAATGGAACCTTCTCATTCC  
GTGAAGAAAAATCTATGAATGGGCGAATGAAACAACTGATTAAGGAAATGCTGGCTGCA  
AACCTCAGGATCGTCCAGATGCTTTTGAAGTGAAGTACAGATTAGTACAAATTGCATTT  
AAAGATAGCAGCTGGGAAACGTGACACATATTATTGCAAATACCATGGATGATATGCTG  
CTTCTGTTTAAACAGTGATGCAACATTATGTGGCTGAAAAAGAATATAAAAAGCTAGACTC  
TACCCTCTAAGGGTTTAGATTTTTTGTGGGATTTTTTTTTTCTCATTCTTAAATCC  
AAGTTGGCCGTTTTATTAGTATGTTTCAAATGTGTATTACCAATGTGGGTGTAAATTTTT  
AAAAATGATTATTGATAGAAGTTTGGCAGGAAAAATCTTTAAGAGCTAACAGAGAAGA  
GAGTCCAGTTTTCTGGAATATGTCTTTAAGTATTTTAGACATTCCCTCGTCAGTATTAGG  
AATTTCCATGGGAAAGAGGTTTGCATGCTGGTAATGCAACCTTTGAACTTTGTAAAGG  
AAACATATATGTATATATTTATGTATATGTAAGTATGTGAATGTGCGCATTTTGCATTCC  
ATATGAAAAAATGCCACGTCTGTTTAAATTATTTGATGTAGGTTTGGGTTTTTGTAGATT  
TGCTGGTGAAGTCAGTGACGAAAAATAAACCTTCCCTTATCTTCCCTACTCTGCCCTCCC  
CCTAATGAAATCATATTAAGTNGTTTTTCCCTNNTTTTTTTTGTAATATACAGCTTTTTTTT  
TAAGGCATCATTTTCGAGGGTCTAAAATTATCTGGTAAACAAATGAAATTAAGTGATCC  
AAAGCTGCTGAAGTATGTTTGAAGTCTCCAGTGCCCTATAGCTGCAAGAGTTGAATTAGT  
CATGCAGTCATATGGCAGCAGGTGGTGATT

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GCGGGGCGCTCCGTATCCCCACGTGGGCCCTGCAGGAACTGGCGGGGCGCGTGACCCGGCG  
AGGCCCAGAGACAGGGGAGGGGCGCCGGGAGCCGGGCGGATCCGCGTCCCCGATGCGCGC  
TGCAATTTCCGGCGGGCGGCGCTGGGGGCGAGCTGGAGCCACCCAGTGCTCGGCCCGCCCC  
GCAACCCGCGCGGAACCGCCGCGCCGAGCGAGGAAGCGCCGCGGGGCGCAGGCGGCCGG  
AATGGCGGGGCGCGGCTGGGGTCCCCCGCGCCTGGACGGCTTCATCCTCACCAGCGCCT  
GGGCAGCGGCACGTACGCCACGGTGTACAAGGCCTACGCCAAGAAGGACACTCGTGAAGT

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## FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT  
CACGGAGATTGAGATCCTCAAGGGCATTTCGACATCCCCACATTGTGCAGCTGAAAGACTT  
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTTGCAGAGGGGGCGACCTGTC  
TCGCTTCATCCATAACCGCAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCA  
ATTAGCTAGCGCCCTGCAATTCTTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCC  
ACAGAACATTCTACTGAGCTCCTTGGAGAAGCCCCACCTAAAAGTGGCAGACTTTGGTTT  
CGCACAAACACATGTCCCCGTGGGATGAGAAGCACGTGCTCCGTGGCTCCCCCTCTACAT  
GGCCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCCCCGCGTGGACCTCTGGTCCATGGG  
GGTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGTGCTTCTCGGA  
GCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCCTTGCGGCCCCCTGCTCTC  
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCCCAGCCGTCGCATCTC  
CTTCCAGGACTTCTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCAGTGGGGAGAG  
TCTGGGGCGAGCAACCGCCCTGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATTCT  
AGCAGCCGCTTATCACTCTACTGCAAGGCTCTGGACTTCTTTGTACCTGCCCTGCACTA  
TGAAGTGGATGCCAGCGGAAGGAGGCAATTAAGGCAAAGGTGGGGCAGTACGTGTCCCG  
GGCTGAGGAGCTCAAGGCCATCGTCTCCTCTTCCAATCAGGCCCTGCTGAGGCAGGGGAC  
CTCTGCCCGAGACCTGCTCAGAGAGATGGCCCCGGGACAAGCCACGCCTCCTAGCTGCCCT  
GGAAGTGGCTTCAGCTGCCATGGCCAAGGAGGAGGCCGCGCGGGGAGCAGGATGCCCT  
GGACCTGTACCAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGCGGAGCCCCCGGGCCGG  
AGGCGGGAGCTGCTTCACACTGAGGTTTCAAGACCTCATGGCCCGAGCTGAATACTTGAAG  
GAGCAGATGAGGGAATCTCGCTGGGAAGCTGACACCCTGGACAAAGAGGGACTGTGGAA  
TCTGTTTCGTAGCTCTTGCAACCTTCAGTGACCCTAGAAGAATGATTGGACAGATGTGAGC  
CATCTGGAGCAGAGGGGCACTAACCAGGCTGACGCCAAGAATGAAGTGGCCCACTGCAG  
CCCTGGCGAGCAGGCTTCTTGGATGGACAGTGTGAGACCCCCATATCCCAGAGTCCCCA  
GCCTCCCTCAGGTTACTCTGCACCCCCACAGATGGTTTGATGGCTGTGCTGTATACTGGAG  
GGGAGGGCAGGACTCTGGGAGAACAGCACTTCTTTCATGAGACCTTTGTTACTCGGTGGT  
TACTGGGTCTGTGCCTGTCCGTTTTGGGGCATGCAGCCCTCTATCATTTTTTGGCTCCGA  
GAAGAGGGCAAGGGGCCCCCGCAGGGTACTTCTGTGCTTGCCCTCGCCCTGCCAGCAGGC  
AGCTGTGCCCTGGCCTGCCCTTCCCGGGACCCCTTATTCCAACCTCAGCTCCTCTTTGCA  
CTGGAATGGGGCACTCCAACACCCCTCAGGGACCACCCTCCCCACAGTATGCACTCAGCC  
CCACAGAACCACAGTCTTTCTGGGAACTCACACCTGCCCGCCATCTTGGTACTTTAGG  
TTAATCCCTCAAGCATGAAAGCTGGATCTTTTGGGGTTTAAGAAGCCCAAGCCTTGTTCC  
TGCCCTGGCCTAGGGAGCACTCAGGAGGGTTCCTTGGTCTCATCTCTCCACCTCCGTT  
CCCTCTGGGCCCCACACTAGCCACAGCGCGGGCCTTGTGCTGGAGTTTGAGCCTGGGACA  
GGGAGAGGGAGGCTTGGAGACAGTCTGACCCAGTGCCCTCTAGGCCACCCACTTCTAGGC  
CTGCCCTGCCGCGTGGAGCCCTGGGCAAGCTCTTTCCCTTTCTGGGCCTGGGTCTCCC  
CATCTCTTCAATGGGGCTGATACCTTCACAGCCCACAGCATGGGCACCTTATGAGGACAAA  
GTGAATTTAACCTGGAAAAGAATGTATTTGAGAGTTTCTTTTAAATAATCAGCGGGTGT  
GGTGATTTGTAGCCCTTCTGCCCTTAAATGCTTCTTGGGCAAGAGCTGTCTGTCTCTCC  
TGCAGGAGGCTGAGTGTGAAGAGTATCATTATTGTTTCTCTATTAAATTATTTTCTCT

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TGGACCTGTCCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACT  
GGACTCTTTTCTTGACTTAGCTACCAGGAGCTAGAGATGCTGTTATTCTATCGTATGTGA  
GAAGTCGGCCAGAGATGGAAAACCTTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAG  
ACTGTTGTCTATAAAGGGCGACGGAAGGGAACAATCAATTTGTAGCCATTCTTTGTACT  
GATAAGTGCAGAAGGCCTGAAATAACCAACTGGGTCCGTCTCACCCTGAAATAAAACAC  
AAGAATATTGTAACCTTTTCATGAATGGTATGAAACAAGCAACCACCTCTGGCTAGTGXAT  
GAAAACCTCCAGAGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGGATTACAT  
CATCTTCATAAACTTGGCATTCTCTTTTGTGACATTTCTCCTAGGAAGATACTCTTGAA

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## FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTGTAGCAACTTTTGCTTGGCAAAGTGAAGGTGAAAATTTG  
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGAGGTGATAATGGGGAAAATGTC  
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT  
GTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTAT  
GAAATGTTTTTCAGGAAAACCTCCATTCTTCTCAGAAAAGTGTTCAGAAATTAAGTGAAG  
ATCTTATGTGAAGATCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCTAAAGCTTCT  
TCAGATTTTATTAATTTGCTTGATGGGTTACTTCAAAGAGATCCTCAGAAAAGATTGACT  
TGGACAAGGCTACTGCAGCATTCAATTTTGAAGAAAGCTTTTGCTGGAGCAGATCAGGAA  
TCAAGCGTGAAGATCTCAGTCTCAGCAGAAACACTATGGAGTGTCTGGGCCACAAGAT  
TCCAAGGAGCTTTTGAGAACTCTCAGAGTAGACAAGCAAAGGGCACAAGAGTGGTCAA  
CCACTAGGTCACCTTTTTCAGACTAGAAAATCCAAGTGAATTTTCGGCCTAAGAGTACTCTT  
GAGGGTCAATTGAATGAATCCATGTTTCTTCTCAGTCTCTCGTCTACTCCAGAACTAGC  
ACTGCAGTGAAGTAAGTCTGGTGAGGATATGACTCACTGTTCAACAGAAAGACTTCT  
CCTCTGACCAAGATTACAAGTGGACACCTGAGTCAGCAGGACCTGGAATCCAGATGAGA  
GAGCTTATCTACACGGACTCAGATCTTGTGTGACCCCCATTATCGACAATCCAAAGATA  
ATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTCACTG  
GATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTTGCAACAAGTGTGCTCG  
CAGATCGACTCCACTGAGAAGAGCATGGGGGGCTCCCGAGCCAAGCTGAATCTCCTTTGC  
TATTTGTGCGTGGTGGCTGGTCACCAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCTG  
TTCCAATTGCTAATCCAGCATTGCGGATAGCTCCAAACTGGGATATACGGGCCAAGGTT  
GCTCACGTGATTGGTTTACTGGCTTCGCACACAAGTGAAGTCCAGGAAAATACACCTGTT  
GTTGAGACTACAAGCTCCATTGGAATCGGGATTTTGAAGTGTCTTGTTCACACTCCACT  
CCAGTGCCTAGACAGTGCCTTGTGTATGTATAGATACTGACAAATATTTCAAATAAATA  
AAACTGTATCAGCATT

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TCTTTGGCCACGTGCTGAGGGCGCGGCAGATCCTGACGGAGCCAGAAGTGCAGGACTAC  
CTGCGGGGGCTGGTCAGCGGCCTGCGCTACCTGCACCAGCGGTGCATCCTGCACCGC

SEQ ID NO: 103\_AA210451\_M SGK384\_M

GGTCTGCTGCATGGATAATGGACTGGAACACAGAAAGACCATGCAGGGTTTCGGCTGTAGA  
AGGCCAGTATCTCCAGAGGCCAGAAGACACCATCAGATCTCCTGGGACTGGAGTTATAGA  
GGTTGTGAGCTGCCATGTTGAACCAAGCAGGTCACTGAGGGACACAGGCATGTGGATGGA  
AACCCTGCTGGGAGAAAAAAGAACTGCTGAAGGGACTGACATGGGACAGCAACATGGAA  
CCAGGAATGGTCTCACGCATAGAGAGCTCCCCGGGGCGTGGGGCTGCTGCTCGCCATGG  
CCCTTATGAACGTGGCGCTCTACCTCTGCCTTGATCAGCTTTTCATCTCCCTGGACGAT  
CCACCGCGGACTCTAGGCGCTGTCCTCCGGGCTACTTCAGAATGGGGCGGATGAGAACT  
GCTCACGCTGGCTGTCTGTGAAGAGCTGAGGACAGAAGTCAGGCAGCTGAAGCGCGTTG  
GGGAGGGAGCCGTGAAGAGAGTCTTTCTGTCTGAATGGAAGGAACACAAAGTCGCTCTCT  
CCCGGCTCACCAGGCTGGAGATGAAGGAGGACTTCCTGCATGGGCTGCAGATGCTGAAGT  
CTCTACAGAGTGAGCACGTGGTCACGCTGGTGGGCTACTGTGAGGAAGATGGCACTATTC  
TCACCGAATATCACCCCTTAGGTTCTTGAGCAACCTGGAAGAAACACTAAACCTTTCAA  
AGTACCAAGACGTGAACACTTGGCAGCACAGGCTGCAGCTGGCCATGGAGTACGTCAGCA  
TCATTAATCTATCTGCATCACAGCCCCCTGGGACAGGGGTCTGTGTGACTCTAACGACC  
TGCCCCAAAACATTGTCCAGTACCTGCTAACAAGTAACCTTCAGCATTGTGGCAAACGACC  
TGGACGCTCTGCCCCCTGGTAGACCATGACTCTGGGGTACTTATAAAGTGTGGCCACAGAG  
AGCTCCATGGGGATTTTGTGGCTCCAGAGCAGCTGTGGCCCTACGGAGAAGACACGCCCT  
TCCAAGACGATCTCATGCCTTCCTACAATGAGAAGGTTGACATCTGGAAGATTCCAGATG  
TCTCCAGTTTCTCTTGGGGCACGTGGAAGGGAGTGATATGGTTAGATTCCATTTGTTTG  
ATATCCATAAGGCGTGCAAGAGCCAGATCCCGGCAGAAAGACCCACTGCTCAGAACGTGC

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## FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTGCGCAGACGAAAG  
AAATGCTGTAAAAATGAGCCATCGAGTGACGTGCTTGATGGCTGAATGGCATCCCAGCTG  
TTCCGCTCTTGATGATGGAAGAGCTTTGCATGGATGGATGTTGACCCTGGCTGTTGAGCC  
ACGTAGGCTCTCTACGTCTGCCTGCATGTTTGAGTGTCTGCTCTCCTGGCAGCCCGG  
ATGGAAGCTGCCAAGCGAGAAAGCCTGGCTTCAGGATGCTCCCTGGTGAAGATGCAGAGG  
ATTCTGGATCTGCATAGTTTCAAGGGAGTGATCAAACGGTGACCTTGAAGACATGCTGCC  
TGCTTTGGTAACTTTTATAGACTAGTAGGAAACAGAAATCTTTTGGGGGAGGGGGGGAC  
AACCCACTAGTTCCCTCAGAGACAATTTCTTCTCATTGAGAAAGCCCTGTTGGAAGCTGGG  
GATGTTTTAACTCCGTGGCAGGGCACTTGCTAGTTGTGTGCAAAGCCTTGGATCTGACC  
CATGGCATGTGCACACACAAATGCTCAAAGAAAATCCAGACGCCAGAAAGTGTGCCCC  
TTTCTTGTCAATAAGGTCATTGTGTCAGTACCGGAGATGATTTTTTTTATGAAGCGTTTATG  
CTGACTCGTGTCACTGAGCCAAGTGTGCATGGTCGTTAGCTACTTTGTGGGTCTTCTTT  
CTTTCTACCCCTACTTCTTCCCTTTCCACCCCTAACACTAGATAGGAGAGAGAGAGAGA  
AAGGAAAGTGGGCACCTGTTATATTGTTGGACGACTTCTTGCTGATTAAGGGGTGTGAGT  
TCCTTGGAGCAATGATCTTTGCTGCCAAGATATCTCATTTCTTCTTGTCTTCTTCTCGCC  
CACGACCACTTCACAAACACCGACCAACAGCAAACAACCCACCCCGCTTCTCGGGGG  
CCCTAGCACTTATGTACTTCTGAAAAGTCCCCAGAAATTCCAATCATCACACACTCAGAG  
AAACTGTCTGCTGCTGGCAAACTACACCCCTGCTAGAGCATGAGGCAAATCATAGTCAG  
CTGCTGTGGACAGTCTGAAGCAGCCTGGCATCCACACCTGAGATTAAAAACAAAAACATT  
CTTACCTGTGTTTTGTTTTGTTTTAAGAAACCAAAGTGCACCAAGATAGCATGCTCTTG  
AGATTGTGGCTGTCTAGAGATTTTTTGAACAGCAAGTTGAAGGAACCTTTCTTACCTGCCT  
TGAATGGTGTCTTTGAACTTCTGCTGACCTGGAGTTTCTGTGTGAATATTTCTATCCAGT  
GTCCCCCTGTACCGGAAAGTACAAAGTCTGCTCTGGGCTTGCATGCCTGAACACTTTAA  
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCAGCACCTGGGAGACAGGAG  
GAACAGGAGTTCAGGGTTATCCTGGGCTATATACCGTGACCCTGTCTACCCCCACACCC  
CAATAAAAAAACAAAAAGGTC

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GAGGTGGTGGCTGTGCAGATGATGGTGGAAATGCATGGATGACCATTACGCCAGTCAGGCC  
CTGGAGGAGCTGATGCCACTGCTGAAGCTGCGGCACGCCACATCTCTGTGTACCAGGAG  
CTGTTTCATCACGTGGAATGGGGAGATCTCTTCTCTGTACCTCTGCCTGGTGTGAGTTT  
AATGAGCTCAGCTTCCAGGAGGTCATTGAGGATAAGAGGAAGGCAAAGAAAATCATTGAC  
TCTGAGTGGATGCAGAATGTGCTGGGCCAGGTGCTGGACGCGCTGGAATACCTGCACCAT  
TTGGACATCATCCACAGGAATCTCAAACCCCTCCAACATCATCTCATCAGCAGTGACCAC  
TGCAAACTGCAGGACCTGAGTTCCAATGTGCTAATGACAGACAAAGCCAAATGGAATATT  
CGTGCGGAGGAAGACCCCTTTTCGTAAGTCTTGATGGCCCTGAAGCCCTCAACTTCTCC  
TTCAGCCAGAAATCAGACATCTGGTCCCTGGGCTGCATCATTCTGGACATGACCAGCTGC  
TCCTTCATGGATGGCACAGAAAGCCATGCATCTGCGGAAGTCCCTCCGCCAGAGCCAGGC  
AGCCTGAAGGCCGTCTGAAGACAATGGAGGAGAAGCAGATCCCGGATGTGGAAACCTTC  
AGGAATCTTCTGCCCTTGATGCTCCAGATCGACCCCTCGGATCGAATAACGATAAAGGAC  
GTGGTGACATCACCTTCTTGAGAGGCTCCTTCAAGTCTCTGTCGTCTCTCTGACCCCTG  
CACCGGCAGATGGTGCCTGCGTCCATCACCGACATGCTGTTAGAAGGCAACGTGGCCAGC  
ATTTTAGGTGATGCTGGGGACACAAAGGGGGAGCGTGCCCTGAAGCTCCTGTCCATGGCC  
TTGGCATCCTATTGTTTAGTTCCAGAGGGTTTATTATTTATGCCCCCTGGCCTTGCTCCAC  
ATGCACGACCAAGTGGCTCAGCTGTGACCAGGACAGAGTCCCTGGGAAGAGAGACTTTGCC  
TCCCTGGGGAACTAGGGAAGCTGTTGGGCCCCATCCCAAAGGTCTGCCGTGGCCCCCG  
GAGCTGGTGGAGGTGGTGGTCACGACCATGGAGCTACATGACAGGGTCTTCGATGTCCAG  
CTGTGTGCTGCTCCCTGCTGCTGCACCTCCTGGGCCAAGCGCTGGTGCACCAACCCGAA  
GCCAAGGCTCCCTGCAACCAAGCCATCACCTCCACCCCTGCTGAGTGCTCTTCAGAGCCAC  
CCCGAGGAGGAGCCACTTCTTGTGATGGTCTACAGCCTGCTAGCCATCACCACAACCCAG

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## FIGURE 2BBBB

GAGTCAGAGTCACTGTGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG  
CACCTCAACAGCTCCCTCGAAAGCAGGGACGTCTGCGCCAGCGGCCTGGGCCTGCTCTGG  
GCCCTCCTGCTGGACGACCCCATCTTGGCACTCCAGCGCCCCAGGAAAAAGAGAGCTCCA  
AACCACGGAAAGCCCCGGGAAACCCAAGAACCCTGCCAGCACCCAAAGTATCATTGTGAAC  
AAGGCCCCCTTGGAGAAGGTCCCGGACCTCATCAGCCAGGTGTTGGCCACCTACCCTGCG  
GATGGGGAAATGGCAGAAGCCAGCTGCGGAGTCTTCTGGCTGCTGTCCCTGCTGGGCTGC  
ATCAAGGAGCAGCAGTTTGAACAAGTGGTGGCGCTGCTCCTGCAAAGCATCCGGCTGTGC  
CAGGACAGAGCCCTGCTGGTGAACAATGCCTACCGGGGACTGGCCAGCCTGGTGAAGGTG  
TCAGAGCTGGCGGCCTTCAAGGTGGTGGTGACAGGAGGGGCGGCAGTGGCCTCAGCCTC  
ATCAAGGAGACCTACCAGCTCCACAGGGACGACCCGGAGGTGGTGGAGAACGTGGGCATG  
CTGCTGGTCCACCTGGCTTCCTATGAGGAGATCCTGCCGGAGCTGGTGTCCAGTAGTATG  
AAGGCCCTGCTCCAGGAGATCAAGGAGCGCTTCACCTCCAGCCTGGTGAAGTACAGCAGC  
GCCTTCAGCAAACAGGCCTCCCTCCAGGTGGAAGCCCCCAGCTGGGGTGCACCACGTCT  
GGGGGACTGGAATAG

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CAGAAGAAGACCCCTGCCAGAAGTCCTGGATGGCTCCTGAAGCTCTCAAATTCTCCTTCT  
CCACCAAATCCGACATCTGGTCTCTGGGCTGCATCATTCTAGACATGGCCACTTGCTCCT  
TCCTGAACGACACAGAAGCCATGCAACTGCGGAAGGCCATCCGCCATCATCCAGGCAGCC  
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT  
TGCTTCTGCCCTTCATGTTGCATATCAACCCCTCCGATCGACTGGCAATCAAGGATGTGA  
TGCAAGTCACCTTCATGAGCAACTCCTTCAAAGCTCCTCTGTTGCGCTGAATATGCAGC  
GGCAGAAGGTCCCCATCTTCATCACTGACGTGCTGCTTGAAGGCAACATGGCCAACATCT  
TAGGCAGCTGGCTGTGTGCTTCTTGTGAACGACAGCAGGCACTGTGACTCAGGGATTG  
GCTCGCAGAGACTTGGGTTTGATTTTTCAGTCAGTCTCTTGGACAGAGCACCCCTCTGAAAG  
ATGTCATGCAGAATTTCTCCAGTCGACCAGAGGTCCAGCTCAGAGCCATTAACAAGTTGT  
TGACAATGCCAGAGGACCAGCTAGGGCTGCCATGGCCACAGAGCTGCTGGAAGAGGTGA  
TCAGCATCATAAAGCAGCATGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCCTTC  
TGCTGCGTGTCTTGGCCAAGCACTGGCAAAGGACCCAGAAGCTGAGATCCCAAGGAGCA  
GTTTGATCATCTCCTTCTGATGGATACCTTGCGGAGCCATCCTAACTCTGAAAGGCTTG  
TTAATGTGGTCTACAACGTGCTTGCCATTATTTCCAGCCAAGGACAGATCTCAGAAGAGC  
TGAAGAGGAGGGGTTGTTTCAGCTTGCCCAAGAGAACCCTGGAGCACTTCCAAGAGGACA  
GGGACATCTGCCTCTCTATCCTGAGCCTGCTCTGGTCCCTCCTGGTAGATGTTGTCACTG  
TGGACAAAGAGCCCTTGGAGCAGCTCTCTGGCATGGTACCTGGGTGCTGGCTACTCATC  
CGGAGGACGTGGAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCTTGTG  
GCTGCATAAAGGAGAGTCAGTTTGAGCAGGTGGTAGTGCTGCTCCTGAGAAGCATCCAGC  
TGTGCCCTGGCAGAGTACTGCTGGTGAACAATGCATTCCGTGGCTTGGCCAGCCTCGCAA  
AGGTGTCCGAACCTGGTGGCCTTCCGAATAGTAGTACTGGAAGAGGGCAGCAGCGGCCTCC  
ACCTCATCCAAGATATCTACAAGCTCTACAAGGATGACCTGAGGTGGTGGAGAACCTCT  
GCATGCTGTGGCCCATCTGACCTCCTACAAGGAGATCCTGCCAGAGATGGAGTCTGGAG  
GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT  
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG  
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCTCTTCAGGC  
CCTGACATGCTGCCCTTCTGGTCTGTGGTAAGAGAAAGTATCACTAGGTCCAGTATTAA  
TTTCGTACCCCATGGTGAATAAAGAAGCCCTAGGCTGTTTCTGGC

SEQ ID NO: 106\_018653.9\_H  
GGCCGGGGTGGGGCGCGGGGCATGCGCGGGGCTGGGCAGGGGGCCGGCGGGGGCGCAGA  
GCGGAGCCGCCTCGGAGCCTGAGCCGCCCGGGGCGGGGCGGGGAGCCGCGCGGGGCGG  
GCCGCGGGGGGAGGGGAGCGATGCGGCGCGGGCGGGCGGCAGTGGCCGCGGGTTTCTG

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## FIGURE 2CCCC

CGCCTCCTTCTGCTGGGCTCCGTCCTCAACGTGCTCTTCGCTCCGGGTCTGGAGCCTCCG  
AGGCCAGGCCAGTCCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTGCGGGGGCCGC  
GGGGAGCTGGCCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG  
GGCCCCGGGCCCCGGGGCGGGCCGGCCGGAGCGGCGGGCGEETGATGGACCTGGCTCCGGGC  
GGGGCCGGCCTGCCGCGCCCCCGGCCCTTGGGCCCCGGCCCCCTGTCCGACGGCGCCCCA  
GGCTGGCCCCCGGCTCCCGGCCAGGCTCCCCCGGCCCGGGCCGCGCCTGGGCTGCGCC  
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC  
CGGGTCCGCTGCCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC  
GATCTGGGCAGCTGCGTGCGCGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC  
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGCTGCGGCACCCCCAACGTGCTGCAG  
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCCAGACACCCTGACCACCATCAG  
GAGCTGGGCGCCCCCTGTAGAAATGATCCAGCTGCTGCAAACCTTCCTGGGAGGATCGATT  
CGAATCTGCCTGAGCCTGGGCGCCTCCTCCACCACCTGGCCCCACTCCCCACTGGGCTCC  
GTCACCTCTGCTGGACTTCCGCCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG  
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA  
CTCGAGTTTTCCGGCCAGGAACCTTACCCTGCCCTGCTCAGCCCAGGGCTGGTGCGAGGGC  
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGGTTTTTCTTCACATACCTCCTGCCT  
CACAGTGCCCCGCCTTCACTGCGTCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG  
CTCGCCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG  
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACAGTGTATCCCA  
GACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC  
CTCCTTTCACTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCCAGTGT  
CGGGCCTTTGTGGTACCAACCAGACCACCTGGACAGGTCCGCAGCTGGTCTTTTTCAAG  
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC  
TGACCTATCTGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCCCTGTG  
GAGGGAGTGAATGCACTGGCAGCACTGCATGTACCTGGGAACCCCTGCAGACAAAGCT  
AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAT  
GTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTAT  
GACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGC  
TGTGCCCTCCTTGGGACGGTTCCTGTTGGGACGCCCCATCACTGTGTTCAATAGTGTGAGA  
ATGTAGCTAAAGCCCCCTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGGTGCG  
TGGGGACAATCCATCGTGGAGTGTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGG  
AGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAG  
GGGACACTCCAGGCCAGCCAGGGGTGAGGGGCAGAGGTGCACACCTCAGCATGAGCCA  
AGACTGGGGTCAGGGAGCAGGTGTGGTTTGAAGCAGGACCTGGGGCGGGGTGGGGCCGG  
GGCCTTTCTGCCTCATTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCC  
CCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTGGTTAAATTGTTTAT  
TTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACCTCTCCC  
T

SEQ ID NO: 107\_AA396601\_M

CCACGCGTCCGGGCTGCGCCGCGCTCCGCAACGTGTCTGGCGCGCAGTACGTGGGCTCAG  
GCTACACTAAGGCTGTGTACCGGGTCCGCTGCCCGGCGGCGCCGCGGTGGCGCTTAAAG  
CAGTGGACTTCAGCGGCCACGATCTGGGCAGCTGCGTGCGCGAGTTCGGGGCGCGAAGGG  
GCTGCTATCGCCTGGCGGCCCAAGCTGCTCAAAGAGATGGTGCTGCTGGAGCGGCTGC  
GGACCCCAACGTGCTGCAGCTCTATGGCTATTGCTACCAGGACAGTGAGGGCATCCCAG  
ACACGCTGACCACCATCACAGAGCTGGGTGCCCTGTGGAGATGATCCAGCTGTTGCAGA  
CTTCTGGGAGGATCGATTCCGAATCTGCCTCAGCCTTGCCCGCCTCCTCCACCACCTGG  
CCACTCCCCGCTGGGCTCGGTACCCCTGCTTGACTTCCGCCCTCGGCAGTTTGTGCTAG  
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCGCGTGGAAGAGACACCGTGCA

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## FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACTTCAGCCTGCCCTGCTCGG  
CCCAGGGCTGGTGCGAGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT  
TCTTACATACCTCCTGCCACACAGTGCCCCGCCTTCCCTCCGACCTCTCCTGGATAGCA  
TCGTCAATGCCACGGGAGAGCTCGEETGGGGGGTGGATGAGACCCTGGCCCAGCTGGAGA  
CAGCGCTACACTTGTTCCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG  
AGTACCAGCGCATCCCGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT  
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG  
AGAGCCATGCTCAGTGTCGTCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTTCGGA  
AGCTGGTCTTTTTTAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGGCAAGACCACAT  
ATGTGAAGGCCCCCTGGTTGACTGGTTGTGGGCTCAGCTGACCAGCTGGGCTTGCCTGCTG  
CAGGCGTGACTTGTCATCCCACCTGGGAACCCCTGCAGACAAAAGCTAGCTCCCAGAGCAA  
CTGATGTGACCAGGACAAAACGTGCAATATGCAAAAATGTTAAAATGTGAGTTTGCCAGC  
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG  
CTCAGGCTGGTCTTAAGTGGGACAGTCCCGTGGGCAGCCATTACTGCATTTCATGCTTTG  
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC  
AACCAGTCTCAGAGTGCTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG  
GAGATGTGAGTGAAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC  
CTAGGCCAGCCCCGAGGCCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG  
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTCGGGGCCTCTCTG  
CCTCATTTGCTTTTCAGTGAAAGCCAGGGAGCAGCCGAGCCAGGCTCCTCCACTCCTGG  
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTGCGTACC  
CAGAAGCTTTTATACCTCTCGTTTCAATAATTGTTTATTTTGTAAAAAAAATTAAT  
CAATTAATAAAAATGATGTTTTGTGAC

SEQ ID NO: 108\_VRK3\_H

ATGATCTCCTTCTGTCCAGACTGTGGCAAAAGTATCCAAGCGGCATTCAAATTCTGCCCC  
TACTGTGGAAATTCTTTGCCTGTAGAGGAGCATGTAGGGTCCCAGACCTTTGTCAATCCA  
CATGTGTATCCTTCCAAGGCTCAAAGAGAGGGGCTGAACTCCAGTTTTGAAACCTCTCCT  
AAGAAAGTGAAATGGTCCAGCACCGTCACTCTCCCCGATTATCCCTCTTCTCAGATGGT  
GACAGTTCTGAGTCTGAAGATACTCTGAGTTCCTCTGAGAGATCCAAAGGCTCCGGGAGC  
AGACCCCCAACCCCCAAAAGCAGCCCTCAGAAGACCAGGAAGAGCCCTCAGGTGACCAGG  
GGTAGCCCTCAGAAGACCAGCTGTAGCCCTCAGAAGACCAGGCAGAGCCCTCAGACGCTG  
AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCACAGGGACAGTGCTGACAGAC  
AAGAGTGGGCGACAGTGGAAGCTGAAGTCCTTCCAGACCAGGGACAACCAGGGCATTCTC  
TATGAAGCTGCACCCACCTCCACCCTCACCTGTGACTCAGGACCACAGAAGCAAAAGTTC  
TCACTCAAACCTGGATGCCAAGGATGGGCGCTTGTTCATGAGCAGAACTTCTTCCAGCGG  
GCCGCCAAGCCTCTGCAAGTCAACAAGTGGGAAGAAGCTGTACTCGACCCCACTGCTGGCC  
ATCCCTACCTGCATGGGTTTCGGTGTTCACCAGGACAAATACAGGTTCTTGGTGTACCC  
AGCCTGGGGAGGAGCCTTCAGTCGGCCCTGGATGTGAGCCCAAAGCATGTGCTGTGACAG  
AGGTCTGTGCTGCAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCTCCATGAGAAT  
GAGTATGTTTATGGAAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT  
CAGGTGACTTTGGCAGGCTATGGCTTCGCCTTCCGCTATTGCCCAAGTGGCAAAACACGTG  
GCCTACGTGGAAGGCAGCAGGAGCCCTCACGAGGGGGACCTTGAGTTTATTAGCATGGAC  
CTGCACAAGGGATGCGGGCCCTCCCGCCGACGACCTCCAGAGCCTGGGCTACTGCATG  
CTGAAGTGGCTCTACGGGTTTCTGCCATGGACAAATTGCCTTCCCAACACTGAGGACATC  
ATGAAGCAAAAACAGAAGTTTGTGATAAGCCGGGGCCCTTCGTGGGACCCTGCGGTAC  
TGGATCAGGCCCTCAGAGACCCTGCAGAAGTACCTGAAGGTGGTGATGGCCCTCACGTAT  
GAGGAGAAGCCGCCCTACGCCATGCTGAGGAACAACCTAGAAGCTTTGCTGCAGGATCTG  
CGTGTGTCTCCATATGACCCCATTTGGCCTCCCGATGGTGCCTAG



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## FIGURE 2EEEE

SEQ ID NO: 109\_S71575\_M VRK3\_M

CCATCCCCACCTGTATCGGCTTTGGCATTACACAGGACAAGTACAGGTTCTAGTATTCC  
CCAGCCTGGGGAGGAGCCTTCAGTCAGCCCTGGATGACAACCCAAAGCATGTGGTATCAG  
AGAGATGTGTGCTTCAGGTGGCCTGCAGGCTGCTGGATGCTCTGGAGTATCTCCATGAAA  
ATGAGTATGTTACAGGGAACCTGACAGCTGAGAATGTCTTTGTGAATCCAGAGGATCTGA  
GCCAGGTGACCCTGGTGGGCTATGGCTTCACCTACCGATACTGCCCAGGTGGCAAACACG  
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG  
ACCTGCACAAGGGATGCGGACCCTCCCGCCGACGCGATCTCCAGACCTTGGGCTACTGTA  
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA  
TAACTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC  
GCTGGAACAAGGCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGTATGGCCCTCAATT  
ATGAGGAGAAGCCACCCTATGCCACGCTGAGGAACAGCCTAGAAGCTCTGCTGCAGGATA  
TGCGGGTGTACCCCTATGACCCTCTGGACCTCCAGATGGTGCCTTAGATGGAATCCAGAG  
CTTCCGACTTGCAGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGA  
CATAGCTCCTAAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA  
TCAGCACTTGTGTTGGGGAACCTGAGTCATGTTCATGTAATGTGAAACTCCTCCCTGTCTC  
AGCTCTGGCAGCTGTGGATGGAGGTAAGTGGATGCTGGCGGCGGCGGCGGCAGCAGCCAC  
TCCACTCCCTATGGCATTCTGTGATGGCATAATAAACTGTTTTTAATC

SEQ ID NO: 110\_AA45427\_H

ATGGGCCACGCGCTGTGTGTCTGCTCTCGGGGAACCTGTCATCATTGACAATAAGCGCTAC  
CTCTTCATCCAGAAACTGGGGGAGGGTGGGTTTCAGCTATGTGGACCTAGTGGAAGGGTTA  
CATGATGGACACTTCTACGCCCTGAAGCGAATCCTGTGTACGAGCAGCAGGACCGGGAG  
GAGGCCCAGCGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTTCGCCTC  
GTGGCTTACTGTCTGAGGGAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTC  
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG  
ACCGAGGATCAAATCCTTTGGCTGCTGCTGGGGATCTGCAGAGGCCTTGAGGCCATTCAT  
GCCAAGGGTTATGCCCACAGAGACTTGAAGCCCAACCAATATATTGCTTGGAGATGAGGGG  
CAGCCAGTTTTAATGGACTTGGGTTCCATGAATCAAGCATGCATCCATGTGGAGGGCTCC  
CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCAGCGGTGCACCATCTCCTACCGAGCC  
CCAGAGCTCTTCTCTGTGCAGAGTCACTGTGTTCATCGATGAGCGGACTGATGTCTGGTCC  
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTC  
AAGGGTGACAGTGTGGCCCTTGCTGTGCAGAACCAACTCAGCATCCCAAAAGCCCCAGG  
CATTCTTCAGCATTGCGGCAGCTCCTGAACTCGATGATGACCGTGGACCCGCATCAGCGT  
CCTCACATTCTCCTCCTCAGTCAGCTGGAGGCGCTGCAGCCCCAGCTCCTGGCCAA  
CATACTACCCAAATCTGA

SEQ ID NO: 111\_H05721\_H

CCCTGAGGCACCGCCCCAAGTTTGGTGTGACCGGCGGGGGACGCCGGTGGTGGCGGCAGC  
GACGGCTGCGGGGGACCGGGCCGCGGCGCCACCATGGCGGTGCGACAGGCGCTGGGCCG  
CGGCTGACAGCTGGGTGAGCGCTGCTGCTGCGCTTCACGGGCAAGCCCGGCCGGGCTA  
CGGCTTGGGGCGGCGGGCCCGGCGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC  
CGCAGGACCGGGCGCGGAGCCTCGCAGGGTCGGGCTCGGGCTCCCTAACCGTCTCCGCTT  
CTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTGTCAGCGGCAGTTCGTGGTGCGGGC  
CTGGGGCTGCGCGGGCCCTTGCGGCGGGCAGTCTTCTGGCCTTCGGGCTAGGGCTGGG  
CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTGAGGAGATCCA  
GGCAATTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTGGACACGAGACGCTTGCA  
GGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGTCTG  
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAGAGCACC  
GTTGCTTCCAGGGAGAGGCCAGGTACCAAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCC



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## FIGURE 2FFFF

GGGGGCCCCCTGCCTTCCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCCCTC  
CAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCCTT  
GGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAGGTCCCAAGCAACTAGC  
CCCTCACCCCAACAATCATCCGGGTTCTCCGCGCCTTCACCTCTTCCGTGCCCTGTGCTGCC  
AGGGGCCCCCTGGTCGACTACCCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGG  
CCATGGCCGGACGCTGTTCCCTCGTTATGAAGAACTATCCCTGTACCCTGCGCCAGTACCT  
TTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGCTGCAGCTGCTGGAAGG  
CGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGACAACATCCT  
TGTGGAGCTGGACCCAGACGGCTGCCCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCCT  
GGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGTACGTGGATCGGGGGCGG  
AAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCCGTCTGGCCCCAGGGCAGTGTAT  
TGAATACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGGCT  
TGTCATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCCGAGCTACCAAGAGGC  
TCAGCTACCTGCACTGCCCCGAGTCAGTGCCTCCAGACGTGAGACAGTTGGTGAGGGCACT  
GCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCGCAAATGTGCTTCATCT  
AAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGG  
CTGGCTCTCCAAACAATCGGCCGCCACTTTGTTGGCCAAACAGGCTCACAGAGAAGTGTG  
TGTGGAACAAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGTGTGAAACGCTCTGCCA  
GGCAGCCCTCTCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGT  
GAATTACTAAAAGAACATGGCATCCTCTGTGTCGTGATGGTCTGTGAATGGTGAGGGTGG  
GAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGAAAAGGCCCTCGGGCTTGG  
CAAATGGAAGAAGCTTGAGTGAGAGTTTCACTGTCAGTCTCTGCTCACAGACATCTGAAA  
AGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATC  
CACAGAGAGGATCCAGGCCAAGGCCTGGCTGTGAGTGGCAGAGTTTGGCTGTGACCTTT  
GCCCCAACACGAGGAAGCTCGTTTGAAGGGGGCAGCGTAGCATGTCTGATTTGCCACCTG  
GATGAAGGCAGACATCAACATGGGTGAGCAGCTTCAAGTTACGGGAGTGGGAAATTACATG  
AGGCCTGGGCCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATC  
TCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTGTGGGGATTTAACTTGAG  
GGTTTCCCTCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAAATGCAAATTTACA  
ACTGCAGATGACGTATGTGCCCTTGAAGTGAATTTGGCTTTAAGAATGATTCTTCTTAT  
ACTCTGAAGGTGAGAATATTTTGTGGGCAGGTATCAACATTGGGGAGAGATTTTCAATGTC  
TAACTAACTAACTTTATACATGATTTTGAAGGCTATTGCCTAAATCAGCGTCAACATG  
CAGTAAAGGTTGTCTTCAACTGACAAA

SEQ ID NO: 112\_AI086865\_H

AATGAGATGGAGAAGTACGAGCGGATCCGAGTGGTGGGGAGAGGTGCCTTCGGGATTGTG  
CACCTGTGCCTGCGAAAGGCTGACCAGAAGCTGGTGATCATCAAGCAGATTCCAGTGGAA  
CAGATGACCAAGGAAGAGCGGCAGCCAGAAATGAGTGCCAGGTCCCTCAAGCTGCTC  
AACCACCCCAATGTCATTGAGTACTACGAGAACTTCTGGAAGACAAAGCCCTTATGATC  
GCCATGGAATATGCACCAGGCGGCACTCTGGCTGAGTTCATCCAAAAGCGCTGTAATTCC  
CTGCTGGAGGAGGAGACCATCCTGCATCTTCTGTCGATCCTGCTTGCACTGCATCAT  
GTGCACACCCACCTCATCCTGCACCGAGACCTCAAGACCCAGAACATCCTGCTTGACAAA  
CACCGCATGGTCGTCAAGATCGGTGATTTCCGGCATCTCCAAGATCCTTAGCAGCAAGAGC  
ACCCCATGCTATATCTCCCTGAGCTGTGTGAGGGCAAGCCCTACAACCAGAAGAGTGAC  
ATCTGGGGCCCTGGGCTGTGCTCTACGAGCTGGCCAGCCTCAAGAGGGCTTTTCGAGGCT  
GCGAACTTGCCAGCACTGGTGTGAAGATCATGAGTGGCACCTTTGCACCTATCTCTGAC  
CGGTACAGCCCTGAGCTTCGCCAGCTGGTCTGAGTCTACTCAGCCTGGAGCCTGCCAG  
CGGCCACCACTCAGCCACATCATGGCACAGCCCTCTGCATCCGTGCCCTCCTCAACCTC  
CACACCGACGGCAGAGAAGTCCGTGGCCCCCAGCAACACAGGGAGCAGGACCACAGTGT  
CCGCTGCAGAGAGGCATCATGACATTCCGGCAGCGGCAGCAATGGGTGCCTAGGCCAT

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## FIGURE 2GGGG

GGCAGCCTCACTGACATCAGCCAGCCCACCATTTGTGGAGGCTTTGTTGGGCTATGAAATG  
GTGCAGCAAGTGGAGGAGGCCCTGAGCTTCACTACTAGGCTCTGCACCCCTGGACCAG  
GAGCCTCTGCTGAGTATAGACCTGGGCACTGCTCACTCAGCTGCTGTGACTGGTGAGGAG  
GACTTGGGCTCTGGAGATGTAAACAGGTTACCCAGCTGGGAGAGAGGACATCTGCTGGCT  
GGTGTGGCGTCCAGCACTGATGTGTCTACCTTCTCTGAAGGTGACTGCAAGGAGCCTGAC  
AAGTGCTGCTGGAGACACAAGCAGTGCCTGGGCACATCATCTACCCCTTTCGCCTCTGAC  
TGTGTCCGCCACAGCCTGCACCTACACTCTGTCAACCACTGCAACTGTAATTCTAGGCTG  
AAGGACTCTTCAGAGGATAGCAGCAGCTCCCGGGGCGCGGGCCCAACCTGCTCCCATGTC  
ATCGAGTCCCCTTGCTTTGAGCTCACACCGGAGGAGGAGCATGTGGAGCGATTCCGGTAT  
GGCTGGTGCAAAAGCTACAGACCTGTCTGTGGCAGTGATCCACCATCCACTCTACCAT  
GAGTGTGGGGCAGATGATCTAAATGXXAAGAAGAGGAAGAGGAGGAGGAGGAAAAGCAAG  
CCCCCATCCCGACACAGGTGGGGCCCGCCACCGCCTCCCCTGACCTAGGCACAGCATG  
GCCACTGGTACCCCTGACTCCACAGCGCCCATCACCATCTGGCGCTCTGAGAGCCCCACA  
GGGAAGGGTCAGGGCAGCAAGGTGATCAAGAAGGTAAAGAAGAAAAAGGAAAAAGAGAAA  
GACAAGGAGGAGATGGATGAGAAGGCCAAGCTGAAGAAAAAGCCAAGAAAGGCCAGTTG  
ACTAAGAAGAAAAGCCCGGTTAAATTGGAGCCTTCCCCGCCAGACGTGAGCCGATCATT  
AGCGCAAGACAGCTGGCCAGGATGTCCGAGTCCAGCCCAGAAAGCCGGGAAGAGCTGGAG  
AGCGAGGACAGTTACAATGGCCGGGGGCGAGGAGAACTGTCCAGCGAGGATATTGTGGAA  
TCATCATCGCCAGGAAGAGAGAGAACACAGTCCAGGCCAAAAAGACAGGGGCAAAGCCC  
TCACAAGCCAGGAAGGTAAACAAGAGAAAAATCTCCCCAGGATCAAACCCCAACCTCAGT  
TGAGGCCAGGGTGGTCAGGGTGCAGAATAAATGCCATCGAGCCTGTGGCTGGCCCTCTGC  
TGCTGTTCTCTCCCTCCAACCTGGCTGTTTCTTGCGGGGCAAGGGGTGGGCTCAGGGCTG  
CAGGGGTTTCTCAAAGGCAATCCAGCTTTTCACAAAGGAAGCCCATGGGAAGGCAGGTGGG  
AGGGAAAGGAAGGGGCACAGCCCTATTTCTTCTACCTGCTAGGACAAGGTGGAAGAGTG  
TATCTGGGGTGGGAAGGAGGGCTTCCCCTCTCTGCTGCGAGAGACTGGTCTGTGTGAAAT  
CCACTTCTGGGACAGGCAGTACTGTCTGCAGCGATAACCCCAATAAACGGAACTTTTAA  
CCC

SEQ ID NO: 113\_AA836348\_H

ATGTCGGTGCTGGGCGAGTACGAGCGACACTGCGATTCCATCAACTCGGACTTTGGGAGC  
GAGTCCGGGGGTTGCGGGGACTCGAGTCCGGGGCCTAGCGCCAGTCAGGGGCCGCGAGCC  
GGCGGCGGCGCGGCGGAGCAGGAGGAACCTGCACTACATCCCCATCCGCGTCTGGGCCGC  
GGCGCCTTCGGGGAAGCCACGCTGTACCGCCGCACCGAGGATGACTCACTGGTTGTGTGG  
AAGGAAGTCGATTTGACCCGGCTGTCTGAGAAGGAACGTCGTGATGCCTTGAATGAGATA  
GTTATTCTGGCACTGCTGCAGCACGACAACATTATTGCCTACTACAATCACTTCATGGAC  
AATACCACGCTGCTGATTGAGCTGGAATATTGTAATGGAGGGAACCTGTATGACAAAATC  
CTTCGTCAGAAGGACAAGTTGTTTGAGGAAGAGATGGTGGTGTGGTACCTATTTTCAGATT  
GTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA  
AATATTTTTCTGACCAAGGCAAACCTGATAAACTTGGAGATTATGGCCTAGCAAAGAAA  
CTTAATTCTGAGTATTCCATGGCTGAGACGCTTGTGGGAACCCCATATTACATGTCTCCA  
GAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGGGCAGTTGGCTGCGTC  
ATTTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAACCCACTTAACCTGTGT  
GTGAAGATCGTGCAAGGAATTGCGGGCCATGGAAGTTGACTCTAGCCAGTACTCTTTGGAA  
TTGATCCAAATGGTTTCATTCGTGCCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT  
GAACTTCTAGATCGCCCTCTTCTCAGGAAACGCAGGAGGTCAAGCACTGTGACTGAAGCA  
CCCATTGCTGTAGTAACATCACGAACCAGTGAAGTCTATGTTTGGGGTGGTGGAAAATCC  
ACCCCCCAGAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGTGCAGGG  
AATACCCACTTTGCTGTGGTCAAGTGGAGAAGGAACTGTACACTTGGGTGAACATGCAA  
GGAGGCACTAACTCCATGGTCAGCTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCA  
AAGCATGTGGAAGGTTGCAAGGCAAAGCTATCCGTCAGGTGTCATGTGGTGTGATTTTC

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## FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC  
ATGGGGGTGGACAAAGTTGCTGGCCCTGAAGTGCTAGAACCCATGCAGCTGAACTTCTTC  
CTCAGCAATCCAGTGGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTGACACGA  
AACAAGGAAGTCTATTTCTTGGGGGTGTGGCGAATATGGACGACTGGGTTTGGATTTCAGAA  
GAGGATTATTATACACCACAAAAGGTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTT  
CAATGTGGCTGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGCTGGCCTGTGGA  
CTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGCATGTCGGGAATTATCAACCATGAA  
GCATAACCATGAAGTTCCCTACACAACGTCCTTTACCTTGGCCAAACAGTTGTCCTTTTAT  
AAGATCCGTACCATTTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGAGGCCGG  
CTGCTGACCTTTGGCTGCAACAAGTGTTGGGCAGCTGGGCGTTGGGAACCTACAAGAAGCGT  
CTGGGAATCAACCTGTTGGGGGGACCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGC  
GGTGATGAGTTTACCATTGCTGCCACTGATGAGAAAGTATTGAATTCTAAGACCATCCGT  
TCCAATAGCAGTGGCTTATCCATTGGAAGTGTGTTTCAGAGCTCTAGCCCGGGAGGAGGC  
GGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGTCAGCAGGAATCTGAAACTCCTGACCCA  
AGTGGAGGCTTCCGAGGAACAATGGAAGCAGACCGAGGAATGGAAGGTTTAATCAGTCCC  
ACAGAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCTGGCTGGCTTCGAAAG  
GAGCTGGAATAATGCAGAAATTTATCCCCATGCCTGACAGCCCATCTCCTCTCAGTGCAGCG  
TTTTTCAGAACTCTGAGAAAGATACCTTGCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCC  
TCTGAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGGTAAGTGAAGCTTTTGGCC  
TTTGAATCACAACCTAGTCACCTCGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAAC  
ACCACTGACTCCTCCTGCGTGTGCGTGCAGCTCTCTGCAGGTGGAGGTTGA

SEQ ID NO: 114\_R86668\_H, MKK6\_H

ATGAACCTGCTGCTCTCCTACCGCGATGTGCAGGACTACTCGGCCATCATTGAGCTGGTG  
GAGACGCTGCAGGCCTTGCCACCTGTGATGTGGCCGAGCAGCATAATGTCTGCTTCCAC  
TACACTTTTGCCCTCAACCGGAGGAACAGGCCTGGGGACCGGGCGAAGGCCCTGTCTGTG  
CTGCTGCCGCTGGTACAGCTTGAGGGCTCTGTGGCGCCCGATCTGTACTGCATGTGTGGC  
CGTATCTACAAGGACATGTTCTTCAGCTCGGGTTTCCAGGATGCTGGGCACCGGGAGCAG  
GCCTATCACTGGTATCGCAAGGCTTTTGACGTAGAGCCAGCCTTCACTCAGGCATCAAT  
GCAGCTGTGCTCCTCATTGCTGCCGGGCAGCACTTTGAGGATTCCAAGAGCTCCGGCTA  
ATAGGCATGAAGCTGGGCTGCCTGCTGGCCCGCAAAGGCTGCGTGGAGAAGATGCAGTAT  
TACTGGGATGTGGGTTTCTACCTGGGAGCCAGATCCTCGCCAATGACCCCCACCCAGGTG  
GTGCTGGCTGCAGAGCAGCTGTATAAGCTCAATGCCCCCATATGGTACCTGGTGTCCGTG  
ATGGAGACCTTCTGCTCTACCAGCACTTCAGGCCACGCCAGAGCCCCCTGGAGGGCCA  
CCACGCCGTGCCCACTTCTGGCTCCACTTCTTGCTACAGTCTCTGCCAACCATTCAAGACA  
GCCTGTGCCCAGGGCGACCAAGTGCTTGGTGCTGGTCTTGGAGATGAACAAGGTGCTGCTG  
CCTGCAAAGCTCGAGGTTCTGGGGTACTGACCCAGTAAGCACAGTGACCCCTGAGCCTGCTG  
GAGCCTGAGACCCAGGACATTCCTTCCAGCTGGACCTTCCAGTGCCTCCATATGCGGA  
GTCAGCGCCTCAAAGCGCGACGAGCGCTGCTGCTTCTCTATGCACTCCCCCGGCTCAG  
GACGTCCAGCTGTGCTTCCCCAGCGTAGGGCACTGCCAGTGGTTCTGCGGCCTGATCCAG  
GCCTGGGTGACGAACCCGGATTCCACGGCGCCCGCGGAGGAGGCGCGGGGGAG  
ATGTTGGAGTTTGATTATGAGTACACGGAGACGGGCGAGCGGCTGGTGCTGGGCAAGGGC  
ACGTATGGGGTGGTGTACGCGGGCCCGGATCGCCACACGAGGGTGCGCATCGCCATCAAG  
GAGATCCCGGAGCGGGACAGCAGGTTCTCTCAGCCCTGCATGAAGAGATCGCTCTTCAC  
AGACGCCTGCGCCACAAGAACATAGTGCGCTATCTGGGCTCAGCTAGCCAGGGCGGCTAC  
CTTAAGATCTTCATGGAGGAAGTGCTTGGAGGCAGCCTGTCTCCTTGCTGCGGTGCGGTG  
TGGGGACCCCTGAAGGACAACGAGAGCACCATCAGTTTCTACACCCGCCAGATCCTGCAG  
GGACTTGGCTACTTGCACGACAACCACATCGTGACAGGGGACATAAAAGGGGACAATGTG  
CTGATCAACACCTTCAGTGGGCTGCTCAAGATTTCTGACTTCGGCACCTCCAAGCGGCTG  
GCAGGCATCACACCTTGCACTGAGACCTTACAGGAACCTCTGCAGTATATGGCCCCAGAA

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## FIGURE 2III

ATCATTGACCAGGGCCCCACGCGGGTATGGGAAAGCAGCTGACATCTGGTCACTGGGCTGC  
ACTGTCAATTGAGATGGCCACAGGTGCCCCCCTTCCACGAGCTCGGGAGCCCCACAGGCT  
GCCATGTTTCAGGTGGGTATGTACAAGGTCCATCCGCCAATGCCAGCTCTCTGTGCGCC  
GAGGCCCCAAGCCTTTCTCCTCCGAACTTTTGAGCCAGACCCCCGCCTCCGAGCCAGCGCC  
CAGACACTGCTGGGGGACCCCTTCTGTCAGCTGGGAAAAGGAGCCGCAGCCCCAGCTCC  
CCACGACATGCTCCACGGCCCTCAGATGCCCTTCTGCCAGTCCCACTCCTTCAGCCAAAC  
TCAACCACCCAGTCTCAGACATTCCCGTGCCCTCAGGCACCCTCTCAGCACCCACCCAGC  
CCCCCGAAGCGCTGCCTCAGTTATGGGGGCACCAGCCAGCTCCGGGTGCCCGAGGAGCCT  
GCGGCCGAGGAGCCTGCGTCTCCGGAGGAGAGTTCCGGGGCTGAGCCTGCTGCACCAGGAG  
AGCAAGCGTCGGGCCATGCTGGCCGCAGTATTGGAGCAGGAGCTGCCAGCGCTGGCGGAG  
AATCTGCACCAGGAGCAGAAGCAAGAGCAGGGGGCCCCGTCTGGGCAGAAACCATGTGGAA  
GAGCTGCTGCGCTGCCTCGGGGCACACATCCACACTCCCAACCGCCGCGCAGCTCGCCAG  
GAGCTGCGGGCGCTGCAAGGACGGCTGAGGGGCCAGGGCCTTGGGCCTGCGCTTCTGCAC  
AGACCGCTGTTTGCCTTCCCGGATGCGGTGAAGCAGATCCTCCGCAAGCGCCAGATCCGT  
CCACACTGGATGTTTCGTTCTGGACTCACTGCTCAGCCGTGCTGTGCGGGCAGCCCTGGGT  
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GAAGGGGACTCCAGCAGAGCCCAGGGCCAGCAGAGCCCCGCTTCCGGTGGAGCCCGAGCAG  
GGCCCCGCTCCTCTGATGGTGCAGCTGAGCCTCTTGAGGGCAGAGACTGATCGGCTGCGC  
GAAATCCTGGCGGGGAAGGAACGGGAGTACCAGGCCCTGGTGCAGCGGGCTCTACAGCGG  
CTGAATGAGGAAGCCCGACCTATGTCTGGCCCCAGAGCCTCCAACTGCTCTTTCAACG  
GACCAGGGCCTGGTGCAGTGGCTACAGGAACTGAATGTGGATTACAGGCACCATCCAAATG  
CTGTTGAACCATAGCTTCAACCTCCACACTCTGCTCACCTATGCCACTCGAGATGACCTC  
ATCTACACCCGCATCAGGGGAGGGATGGTATGCCGCATCTGGAGGGCCATCTTGGCACAG  
CGAGCAGGATCCACACCAGTCACCTCTGGACCCTGA

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ATGTTTGGGAAGAAAAAGAAAAAGATTGAAATATCTGGCCCGTCCAACTTTGAACACAGG  
GTTCACTACTGGGTTTGATCCACAAGAGCAGAAGTTTACCGGCCTTCCCCAGCAGTGGCAC  
AGCCTGTTAGCAGATACGGCCAACAGGCCAAAGCCTATGGTGGACCCTTCATGCATCACA  
CCCATCCAGCTGGCTCCTATGAAGACAATCGTTAGAGGAAACAAACCCTGCAAGGAAACC  
TCCATCAACGGCCTGCTAGAGGATTTTGACAAATCTCGGTGACTCGCTCCAACCTCCCTA  
AGGAAAGAAAGCCCCACCCACCCAGATCAGGGAGCCTCCAGCCACGGTCCAGGCCACGCG  
GAAGAAAATGGCTTCATCACCTTCTCCCAGTATTCAGCGAATCCGATACTACTGCTGAC  
TACACGACCGAAAAGTACAGGGAGAAGAGTCTCTATGGAGATGATCTGGATCCGTATTAT  
AGAGGCAGCCACGCAGCCAAGCAAAATGGGCACGTAATGAAAATGAAGCACGGGGAGGCC  
TACTATTCTGAGGTGAAGCCTTTGAAATCCGATTTTGCCAGATTTTCTGCCGATTATCAC  
TCACATTTGGACTCACTGAGCAAACCAAGTGAATACAGTGACCTCAAGTGGGAGTATCAG  
AGAGCCTCGAGTAGCTCCCCTCTGGATTATTCAATTCCAATTACACCTTCTAGAACTGCA  
GGGACCAGCGGGTGCTCCAAGGAGAGCCTGGCGTACAGTGAAAGTGAATGGGGACCCAGC  
CTGGATGACTATGACAGGAGGCCAAAGTCTTCGTACCTGAATCAGACAAGCCCTCAGCCC  
ACCATGCGGCAGAGGTCCAGGTCAAGCTCGGGACTCCAGGAACCGATGATGCCATTTGGA  
GCAAGTGCATTTAAAACCCATCCCCAAGGACACTCCTACAACCTCCTACACCTACCCTCGC  
TTGTCCGAGCCCACAATGTGCATTCAAAGGTGGATTACGATCGAGCACAGATGGTCCTC  
AGCCCTCCACTGTCAGGGTCTGACACCTACCCAGGGGGCCCTGCCAAACTACCTCAAAGT  
CAAAGCAAATCGGGCTATTCTCAAGCAGTCACCAGTACCCGTCTGGGTACCACAAAGCC  
ACCTTGTAACCATCACCCCTCCCTGCAGAGCAGTTCGCAGTACATCTCCACGGCTTCCTAC  
CTGAGCTCCCTCAGCCTCTCATCCAGCACCTACCCGCCGCCAGCTGGGGCTCCTCCTCC  
GACCAGCAGCCCTCCAGGGTGTCCCATGAACAGTTTCGGGCGGCCCTGCAGCTGGTGGTC  
AGCCCAGGAGACCCAGGGAATACTTGCCAACTTTATCAAAATCGGGGAAGGCTCAACC  
GGCATCGTATGCATCGCCACCGAGAAACACACAGGGAAACAAGTTGCAGTGAAGAAAATG

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## FIGURE 2JJJJ

GACCTCCGGAAGCAACAGAGACGAGAAGCTGCTTTTCAATGAGGTCGTGATCATGCGGGAT  
TACCACCATGACAATGTGGTTGACATGTACAGCAGCTACCTTGTGCGCGATGAGCTCTGG  
GTGGTCATGGAGTTTCTAGAAGGTGGTGCCTTGACAGACATTGTGACTCACACCAGAATG  
AATGAAGAACAGATAGCTACTGTCTGCCTGTCAGTTCTGAGAGCTCTCTCCTACCTTCAAT  
AACCAAGGAGTGATTACAGGGACATAAAAAAGTGAAGTCCATCCTCCTGACAAGCGATGGC  
CGGATAAAGTTGTCTGATTTTGGTTTCTGTGCTCAAGTTTCCAAAGAGGTGCCGAAGAGG  
AAATCATTGGTTGGCACTCCCTACTGGATGGCCCCTGAGGTGATTTCTAGGCTACCTTAT  
GGGACAGAGGTGGACATCTGGTCCCTCGGGATCATGGTGATAGAAATGATTGATGGCGAG  
CCCCCTACTTCAATGAGCCTCCCCCTCCAGGCGATGCGGAGGATCCGGGACAGTTTACCT  
CCAAGAGTGAAGGACCTACACAAGGTTTCTTCAGTGCTCCGGGGATTCTTAGACTTGATG  
TTGGTGAGGGAGCCCTCTCAGAGAGCAACAGCCCAGGAAGTCCCTCGGACATCCATTCTTA  
AAACTAGCAGGTCCACCGTCTTGCATCGTCCCCCTCATGAGACAATACAGGCATCACTGA

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ATGAATGATAGGAATGAGATTCAAATGGAAGCCAAACTCCAAAGTCTTACCATTATAGCA  
CAGGAAATTCTATGCAGATTCTTTATTACCCTTAGGAGACATGCACGTTTCTTGCTCACT  
AAACTAGGAAGGCAAGGAATGGCAAGGTGAGGAATTACTCACAGCTGTGCTGTGTGCATT  
CTCTGTGGGCCTAGCAGGGAAGGGGACAGCCCTGTGGCAATGGGCATGACACGGATGCTC  
CTGGAATGCAGTCTCAGTGACAAGTTGTGTGTATCCAGGAGAAGCAGTATGAAGTGATT  
ATCGTCCCAACTTTGTTGGTTACTATCTTCCTCATCCTTCTTGGGGTCACTCTGTGGCTT  
TTTATCAGAGAACAAAGAACTCAACAGCAGCGTTCTGGACCTCAAGGCATTGCCCTGT  
CCTCCACCTAGGGACCTAAGCTGGGAAGCAGGACATGGAGGAAATGTGGCTTTGCCACTT  
AAGGAGACATCCGTGGAAAACTTTCTGGGAGCTACCACACCTGCCCTGGCTAAGCTGCAG  
GTGCCGCGGGAGCAACTCTCTGAAGTTCTGGAGCAGATTTGCAGTGGTAGCTGTGGGCCC  
ATCTTTTCGAGCCAATATGAACACTGGGGACCCTTCTAAGCCCAAGAGTGTTATTCTCAAG  
GCTTTAAAGAACACAGCTGGGCTCCATGAGGTACAAGATTTCTTAGGGCGAATCCAATTC  
CATCAATACCTGGGGAAACACAAAAACCTGGTGCAGCTGGAAGGCTGCTGCACTGAAAAG  
CTGCCACTCTATATGGTGTGGAGGATGTGGCCCAGGGGGACCTGCTCGGCTTTCTCTGG  
ACCTGTGCGCGGGATGTGATGACTATGGATGGTCTTCTCTATGATCTCACAGAAAAACAA  
GTATATCACATCGGAAAGCAAGTCCTTTTGGCGCTGGAATTCCTGCAGGAGAAGCATTG  
TTCCATGGGGATGTGGCAGCCAGGAATATTCTGATGCAAAGTGATCTCACTGCTAAGCTC  
TGTGGATTAGGCCTGGCTTATGAAGTTTACACCCGAGGGGCCATCTCCTCTACTCAAACC  
ATACCTCTCAAGTGGCTTGCCCCAGAACGGCTTCTCCTGAGACCTGCTAGCATCAGAGCA  
GATGTCTGGTCTTTTGGGATCCTGCTCTATGAGATGGTGACTCTAGGAGCACCACCGTAT  
CCTGAAGTCCCTCCTACCAGCATCCTAGAGCATCTCCAAAGAAGGAAAATCATGAAGAGA  
CCCAGTAGCTGCACACATACCATGTACAGTATCATGAAGTCCTGCTGGCGCTGGCGTGAG  
GCTGACCGCCCCCTACCTAGAGAGCTGCGCTTGCGCCTAGAAGCTGCCATTAAACTGCA  
GATGACGAGGCTGTGTTACAAGTACCAGAGTTGGTGGTACCTGAACTGTATGCAGCTGTG  
GCCGGCATCAGAGTGGAGAGCCTCTTCTACAACCTATAGCATGCTTTGAAGAGTCTCGGGC  
AAGAAACATTTCATGCATGAGTATATGTTCTTGGAAATCAATTCTCTAAGAACAGAGAATG  
GTCTTTCCCAGGGACACAAAGGGAGAAATGGGACATGGATTCTTGATCTTCTTTTACACA  
TTTCTCGGGAAATCTGAAATGATGCTGGATGGGACTCTACACATCCTGAGCTAAGACATA  
CTGTCACTCTCACTTCTGCTGTCCCAGTCCCTAGAAATCCTGGGTAGAAGTGGTGGACCTG  
TGCAAAGGAGGTTTTAGAACTCTGCAGTATTTGTTGGGGCATGGCACAAATAAGCTCATC  
CCTCCCGTCCGAGGCTAGTTTCTCTGGAACCAATTTTTATCTAGATGAAAATTTGGAA  
TGAAATGAAGGAATAGAAATCCAATAAAAGAGTTGAAGGGAAAGAAAATTTAAGGTTCTT  
CTTGCTCAGGATTACAGATATGGACCAACACCTCCTTCAAGAAAAGGTGGTAGGACACAA  
AGTTCTTCAGTCCCTGAGCCCTACATGTGGGGCTGGAGGAGAACTATAACGGAAAAACCTC  
TGAGTTTCACCTTAGGTATAGATAAAAGAAAGATGGTCCCCTTTTATCTGATTCTGAGAC  
AGGTAAATTCTGTTTGTACTACGTTTAATTAGAAGGTGGAGGAGTCAATTCATGATTAA

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## FIGURE 2KKKK

GAACATTCAACATGTATTGTTTATTAAAGCTAGCTTCCTAGTTCCGATTAGACTAAGGAGA  
CTAAGCCTAGAGAGTCAATGTTAGAACAGTGAAAAGAATTCTGTGTGTGTGTGTGTGT  
GTGTGTGTGTGCAATAAATAGGAAATGTAGAAACCAAGCAAGAAGGCTTAGTAGCTCA  
GTCTTTAAACAAGGGCTAGAAAAGAATGTAATCTGATATGGAAGGATAGCAGCTTCTAATT  
TTCAATCATCTGTTGATATACTGTGAAACTTATTTTATTAAATTAATATTTATTAAATGG

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CTGCAGGAGAAGCACCTGTTTCATGGGGATGTGGCTGCCAGGAACATCCTGATCCAAAGT  
GACCTGACTCCCAAACCTTTGTCTATCTGGGCCTGGCTTATGAAGTTCATGCCCATGGGGCC  
ATCTCCTCTGCTCGATCCAGCACCATCCCTCTCAAGTGGCTTGCTCCAGAAAGGCTTCTC  
CTGAGACCTGCAAGCATCAGGGGAGATATTTGGTCTTTGGGATCCTGCTTTATGAGATG  
GTGACTCTAGGAGCACCACCATACCTGAAGTCCCTCCCACCAGCATCCTACAATATCTT  
CAGAGAAAGAAAATCATGAAGAGACCCAGCAGCTGCTCACATGCCATGTACAACATCATG  
AAGTGCTGTTGGCGCTGGAGTGAGGACAGCCGCCCTTACTTGTTTCAAGCTGCTCCAGCGC  
CTAGAAGCTGCTTCTAGATCTGCCGATGACAAGGCTGTGTTGCAAGTGCCAGAGTTGGTG  
GTGCTGAACTGTATGCAGATGTGGCTGGCATCAGGGCAGAAAGCATTTTCTATAGCTTC  
AGTGTCTTTTGAAGATGGTCTAGACAAATGACTATATATGGGTGGAATTAGTTCCTTCA  
AGAACAGAGAGAAGGAACTTTCTGTGGCCACCAAGGGAGAAAAAAGGACATGGATCTTG  
CATCTTTCCCTAAACATTTTCTAGACATCTGAAATGCTGCTGGATGAAGCTCTACCTCT  
ACATACCATGTACTCTTGAGCTAAGAATCACCATCAATTGTAGTTTGCTTTCCAGTCCCA  
AGGGCTGAAGTATAAGTGGTGGACCGTGTCTATTCTAAAGGAGTTTTTAAATCTGCAAT  
GATTGTAAGGGAATTAGGCAAAGGGCTGGTCCCACTCACTCCAGGCTGGTTTACTACTG  
AAACTAGTTTTTCTTTTCTTTTTTTTAAAGTTAAACTATTACAGAGTAAAAATAAACAG  
ATGGGCATGAATGAACACCTTCTAATTTTTTAACCATGAATTGAATATTGGAATTCATGAG  
AAAGAAAATTCTAGGTTCTTTTTTGCTAAGAGGTGTTAAGGTGAGTCAATATATCCTTCAA  
GGAAAGGCTTTGTCTCATCTATGTTGACGGGACGTAAAAGTCTCGTCCCGTTATGAAGA  
GCTGAAGAAGATCTATAAGAAACAATACTGAGCCTTTCCTTGACTATAGATAGAAGAGCA  
TCCTTTCATTGAACCTCTGAGGCAGGTGGACCATGCATGATACTAAGTTTAATTAGAAGCA  
GGAGGAGTCATTTTCATGATTAGGAACATTGTTTCATCCATTGTTTGCCAGTTCCTGTAA  
GACTAAGGAGAATCAGCCTATAGAGCCAAAGCTAGAACCAGGGATAAAAAGTGTGTGTGT  
GTATAACAAATAGGAAGCATGAAAGTTCGAGCAAGAAGACTTAGTAACCCAGGTGGTCATT  
AAGAGGTACAGAGAAGAAGTAATCTTATAGGAATGGATGGTAGCTTCTAATTTTTTAACCA  
TTCATTGAAATAACTGTGAAGCAACTCATTAACTAGTATTTATTGACCAAAAGTAGACT  
TTTCAGGTGTATAGCTGCCAAAATCTCTATAATAAAGAGGCTAAAAGAAAATAAATGGGA  
GTTATTTTACTAGGAAAATTAGAGAACCTATAGTTTCCAAAAGAGATTCTTTATGTGCA  
AAATGAGATAACTCTCTACCTCACAGGGTTGGTGTGAGGAACAATGAGAAATATGTATTG  
TGTATTATGTAGAATATAATATATTCTCAATAAATACTAGTTTTTCCCCTTC

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GAAGAGGGCAGAGCCGTGCATGGGGCTGCTCCCCAGGACCTGAGCAGGAACCTGGAGTTT  
TCAGAGCTGCCTGATCATTGCTACAGAATGAACTCTAGCCCAGCTGGGACCCCAAGTCCA  
CAGCCCTCCAGGGCCAATGGGAACATCAACCTGGGGCCTTCAGCCAACCCAAATGCCAG  
CCCACGGACTTCGACTTCCTCAAAGTCATCGGCAGGGAAGTACGGGAAGGTCTACTG  
GCCAAGCGCAAGTCTGATGGGGCGTTCTATGCAGTGAAGGTACTACAGAAAAGTCCATC  
TTAAGAAGAAAGAGCAGAGCCACATCATGGCAGAGCGCAGTGTGCTTCTGAAGAAGGTG  
CGGCACCCCTTCCTCGTGGGCCTGCGCTACTCCTTCCAGACACCTGAGAAGCTCTACTTC  
GTGCTCGACTATGTCAACGGGGGAGAGCTCTTCTTCCACCTGCAGCGGGAGCGCGGTTT  
CTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGTGGCCAGCGCCATTGGCTACCTGCAC  
TCCCTCAACATCATTACAGGGATCTGAAACCAGAGAACATTCTCTTGGACTGCCAGGGA  
CACGTGGTGTGACGGATTTTGGCCTCTGCAAGGAAGGTGTAGAGCCTGAAGACACCACA



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## FIGURE 2LLLL

TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTAT  
GATCGAGCAGTGGACTGGTGGTGCTTGGGGGAGTCTCTACGAGATGCTCCATGGCCTG  
CCGCCCTTCTACAGCCAAGATGTATCCCAGATGTATGAGAACATTCTGCACCAGCCGCTA  
CAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGACCTCCTGCAAAGCCTTCTCCACAAG  
GACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTTTCTTGAGATTAAGAACCATGTATTC  
TTCAGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCACCCTTCAACCCA  
AATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTCACCCAGGAAGCTGTG  
TCCAAGTCCATTGGCTGTACCCCTGACACTGTGGCCAGCAGCTCTGGGGCCTCAAGTGCA  
TTCTTGGGATTTTCTTATGCGCCAGAGGATGATGACATCTTGGATTGCTAGAAGAGAAGG  
ACCTGTGAAACTACTGAGGCCAGCTGGTATTAGTAAGGAATTACCTTCAGCTGCTAGGAA  
GAGCGACTCAAACATAACAATGGCTTCAACGAGAAGCAGGTTTATTTTTTCCAGCACATAA  
AAGAAAAATAATGTTTTCGGAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCAGAGGC  
TGTATCTCTGCCCTTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAAATGGAGGAAAGGGGA  
GTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAAATGGAGGAAAGGGGA  
GAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAAAGCTCCCCCAATGACTTTTGCTT  
CCATCTCACTAACCACCCACCCCTACCTGGAATGGAGGCTGGGAAATGTGGCTTATTTGC  
TGGGTACGTGACTATCCCTAATAACAAAGGGGTTTTGACCCTAAGACATTAGGGGAGAAT  
GTTGGGTAGGCAGCCAGCCCTCTTTTACCATAGGGCCTCCTGGTGTGTTGGATTTTGATCT  
CAATGTGTAAATGACAGAGATGTAACAAGCTCATAGGGTATCAATATCTCTTATTGTTC  
TATGTTGAAAAA

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ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGGCGCCACGGCATCGTCTTCAAG  
GCCAAGCACGTGGAGACTGGCGAGATAATTGCCCTCAAGAAGGTGGCCCTAAGGCGGTG  
GAAGACGGCTTCCCTAACCAGGCCCTGCGGGAGATTAAGGCTCTGCAGGAGATGGAGGAC  
AATCAGTATGTGGTACAACCTGAAGGCTGTGTTCCACACGGTGGAGGCTTTGTGCTGGCC  
TTTGAGTTTCATGCTGTGCGATCTGGCCGAGGTGGTGCGCCATGCCAGAGGCCACTAGCC  
CAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTGCTCTTCTGCCATGCC  
AACAACTATTGTACATCGGGACCTGAAACCTGCCAACCTGCTCATCAGCGCCTCAGGCCAG  
CTCAAGATAGCGGACTTTGGCCTGGCTCGAGTCTTTTCCCCAGACGGCAGCCGCCTCTAC  
ACACACCAGGTGGCCACCAGGTCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGGGTCC  
CCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGCTTCGCATCTTGGGC  
ACCCCAAACCTCAAGTCTGGCCGGAGCTCACTGAGCTGCCGGACTACAACAAGATCTCC  
TTTAAGGAGCAGGTGCCCATGCCCTGGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCA  
TTGGATCTGCTGGGTCAATTCCTTCTCTACCCTCCTCACCAGCGCATCGCAGCTTCCAAG  
GCTCTCCTCCATCAGTACTTCTTACAGCTCCCCTGCCTGCCATCCATCTGAGCTGCCG  
ATTCTCAGCGTCTAGGGGGACCTGCCCCAAGGCCCATCCAGGGCCCCCCCCACATCCAT  
GACTTCCACGTGGACCGGCCTCTTGAGGGAGTGCCTGTTGAACCCAGAGCTGATTTCGGCC  
CTTCATCCTGGAGGGGTGAGAAGTTGGCCCTGGTCCCGTCTGCCTGCTCCTCAGGACCAC  
TCAGTCCACCTGTTCTCTGCCACCTGCCTGGCTTCAACCTCCAAGGCCTCCCCATGGCC  
ACAGTGGGCCCCACACCACACCTTGGCCCTTAGCCCTTGCAGGGGTTGGTCTCGAGGCAGA  
GGTCATGTTCCCAGCCAAGAGTATGAGAACATCCAGTCGAGCAGAGGAGATTCTATGGCCT  
GTGCTCGGTGAGCCTTACCTTCTGTGTGCTACTGACGTACCCATCAGGACAGTGAGCTCT  
GCTGCCAGTCAAGGCCTGCATATGCAGAATGACGATGCCTGCCTTGGTGCTGCTTCCCC  
GAGTGCTGCCTCCTGGTCAAGGAGAAGTGACAGAGATAA

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GAATTCGCGGCCGCTCGACGCTCAGCAGAGCTACCAGCTGCCCTGTTGGCTTCGCTGGTC  
GGATCGTCTCCTGGCCCCGCCAAACAGGCGAGCGGCCCGACTGTGGGGCATGGCAGTA  
GTCTCCTCGTTCTCCGCCGCCGCTAGCCTAGCTGAGTCGCCGGCTTCTGCGCTAGGGGCT

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## FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC  
TCCCTCTTTGCCGCGTCTCCTCCTCTTGCCCGCGCAGGCACCCCTCTGGCTGCTCAGTC  
CTGCCTCAGTGTCAAACCAGAAGAGAAGTAAAATTCAACAAAAATTTATGTGTGGAGTTC  
CTTCTTAAAAGAAGAAAAAGTGATTATTTAGACTATGGATCGGAGCAAACGGAATTCAA  
TTGCAGGATTTCTCTCCACGTGTGGAGCGTCTTGAAGAGTTTGAAGGAGGTGGTGGAGGAG  
AAGGAAATGTGAGCCAGGTGGGAAGAGTTTGGCCATCTTCGTATCGAGCTCTTATAAGTG  
CCTTTTCCAGACTGACGCGTTTGGATGATTTACCTGTGAAAAAATAGGGTCTGGCTTCT  
TTTCTGAAGTGTTCAGGTACGACACCGAGCTTCTGGTCAGGTGATGGCTCTTAAGATGA  
ACACATTGAGCAGTAACCGGGCAAACATGCTGAAAGAAGTACAGCTCATGAATAGACTCT  
CCCATCCCAACATCCTTAGGTATATCAACTCCGGGAACCTGGAACAGTTGCTAGACAGTA  
ACCTGCATTTGCCTTGGACTGTGAGGGTAAACTGGCCTATGACATAGCAGTGGGCCTCA  
GCTACCTTCACCTCAAAGGCATTTTTCATCGGGACCTCACATCTAAGAACTGCCTGATAA  
AGAGGGATGAGAATGGTTACTCTGCAGTGGTAGCTGACTTTGGCCTGGCTGAGAAGATCC  
CCGATGTCAGCATGGGGAGTGAGAAGCTGGCCGTGGTGGGTTCCTTCTGGATGGCAC  
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TCCTCTGCGAGATCATCGCCCGCATCCAGGCCGATCCGGACTATCTTCCCCGCACAGAGA  
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TGCAACTTACTTTCAACTGCTGTAACATGGATCCCAAACCTGCGCCCATCTTTTGTGGAGA  
TTGGGAAGACCTGGAGGAAATTCTGAGCCGCTACAGGAAGAAGAGCAGGAGGGGATA  
GGAAGCTGCAGCCACAGCCAGGGGACTCTTGGAGAAAGCACCTGGGGTGAAGCGACTAA  
GCTCACTGGATGACAAGATCCCCCACAAGTCACCATGCCCAAGACGTACCATCTGGCTGT  
CTCGAAGCCAGTCAGATATCTTTTCCCGTAAGCCCCCACGTACAGTGAGTGTCTTGGACC  
CATACTACCGGCCACGAGATGGTGTCTGCCCCGACCCCCCAAAGTCAACCCTTTTAGTGCTC  
GCCAGGACCTCATGGGGGGCAAGATCAAGTTTTTTTGACCTGCCCAGCAAGTCTGTCTCT  
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AGCCCCCTGGCCCCACCTATTCGCCGTTGGCGTTCTTGGCTGGTTCGCCTGAGTCTTGC  
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GCCTAAGTAGTCTCAAGTACAGAGTTAAAGAGATCCACCATTCCGGGCATCTGCCCTAC  
CAGCTGCTCAAGCCCATGAGGCTATGGACTGCTCCATTCTCCAGGAAGAAAATGGTTTTG  
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AAGAAAGGCCAGCAGGCTCAACTCCAGCCACCTTCTCCACCTCAGGCATAGGCCTGCAAA  
CCCAGGGAAAGCAGGATGGGTGAGGGGGTTAGTCCCTGCCTCACCTTGGGGATGGACCT  
TCAGCTGAAACCATATGGCCCCCTAGGTGCACAGCCTTGATTCTTCCCTGGAGCCTACAG  
AGCAGGCAGGCTAGGCCAAGCCAGGCTCAACTTCTGGGCTCCCAGTGCCATTGGCTGTG  
TATGACGGGAGGCAGCAGTGAGAGGCCTTCCTAGTTAGGGCCAACAGCTGATACCAAGCC  
TCTGAAATCCAGCAAGGAGGTCTGCCTCCCACCAGACCCTCTCCAGTGTACTTCCCCAGA  
TAGGACCAGAGGATGTCTAGTTCTAGGCTGAGCTGGCAGGCAGCTATTACCCCGGTTCTT  
TCCCCACCCAGGTCTGTCTCTTGCCTTTTCTTGGGGCATATAAGCTACTGAGTGGAACA  
TGGAGCTGATCAAGAGGCCGTAATGGTTCATGGCTGTTTCCAGACCTGAATATTGGGTGCT  
TCTTGCCAGTATTCTAAGACATTTGAGTAATTGCTGTTTGCACTTACTGCATGGTCAGAC  
CACGTCACTACATTTCTATGCAAGGGGACAGCAAGGCAGCGTGGTGGTTCATGGCTCTTAG  
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CCTTACAGAGCTGCAATAAGAAATAACCAAAGATGAAGCTGGTCAAATATTTTCATAACT  
TGCTTCTGTTGATTTTTTTTTTTGTAAAACCTTTCCCAAGACATTTTCAGACTTAAAAATAA  
AGTCAGTGTTACAGGT